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(54) Title: DEFECTS IN DRUG METABOLISM			
(57) Abstract The invention relates to genetic material, and specifically portions of DNA, for identifying the presence or absence of a mutation in the drug metabolism gene CYP2C9 and CYP2A6. Further, the invention comprises a method for determining such mutations and a kit incorporating the genetic material of the invention for performing the said methods so as to determine the presence or absence of mutations in the drug metabolizing gene CYP2C9 and CYP2A6.			

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DEFECTS IN DRUG METABOLISMFIELD OF THE INVENTION

The invention relates to genetic material, specifically primers, for use in a method designed to determine the genotype of an individual; and also a kit, including the genetic material of the invention, for performing the method of the invention.

BACKGROUND OF THE INVENTION

It is well known that genetic polymorphisms in drug metabolizing genes give rise to a variety of phenotypes. This information has been used to advantage in the past for developing genetic assays that predict phenotype and thus predict an individual's ability to metabolize a given drug. The information is of particular value in determining the likely side effects and therapeutic failures of various drugs. The availability of this sort of information will result in routine phenotyping being recommended for certain categories of patients.

Drug metabolism is carried out by the cytochrome P450 family of enzymes. For example, the cytochrome P450 isozyme gene, CYP2C9 encodes a high affinity hepatic [S]-warfarin 7-hydroxylase which appears to be principally responsible for the metabolic clearance of the most potent enantiomer of warfarin. Similarly, the cytochrome P450 isozyme gene, CYP2A6, encodes a protein that metabolizes nicotine and coumarin and activates the tobacco-specific nitrosamine 4-(methylnitrosamino)-1-(3-pyridyl)-1-butanone) (NNK).

It is of note that the above gene products are also known to metabolize other substrates, for example, the CYP2C9 gene product is also known to metabolize Tolbutamide, Phenytoin, Ibuprofen, Naproxen, Tienilic acid, Diclofenac and Tetrahydrocannabinol.

It follows that genetic polymorphisms or

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mutations in either of the two aforementioned genes can lead to an impairment in metabolism of at least the aforementioned drugs.

In so far as CYP2C9 is concerned, sequences reported by Yasumori et al (1987 *J. Biochem.* 102:1075-1082.) and Kimura et al (1987 *Nuc. Acids Res.* 15:10053-10054) show differences at several positions including a C to T base change that results in a Arginine/Cysteine polymorphism at amino acid 144. This polymorphism has been designated R144C.

In so far as CYP2A6 is concerned, a T to A base change at position 488 of the cDNA sequence described by Yamano et al (1990 *Biochemistry* 29:1322-1329) results in substitution of Leucine 160 by Histidine. Henceforth this mutant form of the gene will be designated CYP2A6v1.

The variant CYP2A6v1 encodes an enzyme that is unstable and catalytically inactive. It is found in the general population at a frequency of about 1% but does not account for all slow metabolizers of coumarin.

Since the cDNA sequence structure of CYP2C9 and CYP2A6 are known, and since it is also known to perform genetic assays to determine whether a preselected mutation is present within a given gene, it should, in theory, be possible to design assays which specifically determine whether either of the aforementioned mutations are present in each of the respective aforementioned genes.

However, we have found an extraordinarily high degree of exon homology in the cytochrome P450 genes. This has resulted in non-specific binding of assay materials and poor performance of assays. In the instance where primers have been used to hybridize to genetic material, non-specific binding of such primers has taken place, and in the further instance where primers have been used to hybridize to genetic material with a view to performing a polymerase chain reactions we have found that related genes have also been amplified, for example, CYP2A7, CYP2A12 and CYP2C8 have also been amplified.

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SUMMARY OF THE INVENTION

The present invention relates to novel variant alleles in cytochrome P450 genes which express enzymes involved in the metabolism of particular drugs and/or chemical carcinogens.

5 One object of the present invention relates to the discovery of new mutant or variant CYP2A6 alleles wherein the human gene is characterized. A new variant allele has been found which is designated CYP2A6v2. The cDNA and genomic sequence of CYP2A6v2 is provided in the present invention. Another new gene related to
10 CYP2A6 has been discovered and is designated CYP2A13. The cDNA and genomic sequence of CYP2A13 is provided in the present invention.

15 Another object of the present invention relates to the use of intron sequences to specifically identify CYP2A6 and CYP2C9 variants in a gene specific detection assay.

20 Another object of the present invention is to use an oligonucleotide probe, specific for regions unique to a particular CYP2 variant to screen for the presence or absence of the variant in a sample.

25 Yet another object of the invention is to provide genetic material, a method, and a kit which enable genotyping of the CYP2C9 and CYP2A6 gene with a view to providing phenotypic information concerning drug metabolism.

30 A further object of the present invention provides a method for diagnostically determining the sensitivity of a patient for specific drugs and chemical carcinogens. Such a method is widely applicable in determining the proper dosage of a drug for a patient.

35 Another object of the present invention provides a method of genotyping CYP2A6 and CYP2C9 and determining whether a mutation has altered the sequence of these genes and hence altered sensitivity to particular drugs and chemical carcinogens.

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In accordance with the present invention a method is provided which utilizes the finding that each variant of a CYP2 gene has specific nucleotide differences as compared with the wild-type CYP2 gene. Such nucleotide changes can be utilized in a probe-hybridization assay, which is capable of specifically detecting a chosen variant and not other variants.

The present invention also provides a genotyping method for identifying the presence or absence of a mutation at codon 144 of the coding sequence of CYP2C9, or alternatively, at codon 160 of the coding sequence of CYP2A6, or alternatively, a gene conversion event involving CYP2A6 and CYP2A7 in exons 3, 6 or 8 comprising use of a portion of DNA. Such a mutation is then correlated to the sensitivity of particular drugs and chemical carcinogens.

The present invention further relates to a gene-specific bioassay which is capable of distinguishing between the CYP2 genes and identify the presence or absence of a mutation in CYP2A6 and CYP2C9 genes. Such a bioassay can diagnostically predict the sensitivity of an individual to particular drugs or chemical carcinogens. For example, the CYP2C9 variants identify a sensitivity to a commonly used anti-coagulant drug, warfarin. The CYP2A6 variants identify sensitivity to coumarin, nicotine and nitrosamines. The sensitivity to nicotine may be used to predict a predisposition to tobacco-related diseases, a propensity to smoking and adverse reactions to exposure to nicotine. Further, CYP2A6 genes are associated with the activation of nitrosamines, elevated levels of which have been correlated with many cancers.

The present invention also provides a method of genotyping the CYP2A6 and CYP2C9 genes using allele-specific amplification reaction.

In addition, a highly-specific combination genotyping bioassay has been developed to identify mutations within CYP2A6 and CYP2C9 which are linked to

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sensitivity to particular drugs and chemical carcinogens. This combination bioassay comprises a gene-specific amplification reaction, an exon-specific amplification reaction and an endonuclease cleavage reaction wherein only one form, either mutant or wild-type is cleaved, producing either a single nucleic acid fragment or multiply nucleic acid fragments depending upon the presence or absence of the mutation. For example, one CYP2C9 variant, R144C, which contains a C₄₇₂→T mutation can be identified by an *Ava*II restriction site. CYP2A6 variants can also be identified by their corresponding mutations. CYP2A6v1 which contains a T₄₈₈→A mutation can be identified by a *Xcm*I restriction site. CYP2A6v2 which contains a T₄₁₅→A mutation can be identified by a *Dde*I restriction site.

The present invention also relates to a method for screening patients for drug sensitivity prior to their treatment with that drug, thereby alerting a physician of a drug sensitivity. In addition, the method may be used to screen patients for a predisposition to cancers related to excessive nitrosamine activation, which are associated with mutations within the CYP2A6 gene locus. Further, the method may be used to screen patients for a sensitivity to chemical carcinogens, based upon the genotype of the CYP2A6 and/or CYP2C9 alleles.

One such new allele variant, CYP2A6v2, has 98% nucleotide similarity and 80% amino acid similarity with the wild type CYP2A6, respectively. The present invention relates to the new CYP2A6v2 variant, the cDNA sequence and its genomic sequence wherein the alterations in sequence are within exons 3, 6 and 8, which are attributed to a gene conversion. In addition, another new gene, also involved in drug metabolism has been identified, and has been designated CYP2A13. This gene plays a similar role in drug metabolism as CYP2A6. These new gene sequences or fragments thereof are used as probes in identifying specific CYP2 variants in samples. In additions,

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fragments of the new genes are used as primers in a genotyping assay.

The invention further provides isolated CYP2Av2 and CYP2A13 cDNAs for use in gene therapy and replacement protocols for individuals who are predisposed to sensitivity to needed drugs or to chemical or environmental carcinogens.

In accordance with an aspect of the present invention, there are provided primary human cells which are genetically engineered with CYP2A6v2 or CYP2A13 DNA (RNA) which encodes a therapeutic agent of interest, and the genetically engineered cells are employed as a therapeutic agent. (The term "therapeutic," as used herein, includes treatment and/or prophylaxis.)

Gene expression in an organism in accordance with the practices of this invention is regulated, inhibited and/or controlled by incorporating in or along with the genetic material of the organism non-native DNA which transcribes to produce an RNA which is complementary to and capable of binding or hybridizing to a mRNA produced by a gene located within said organism. Upon binding to or hybridization with the mRNA, the translation of the mRNA is prevented. Consequently, the protein coded for by the mRNA is not produced. In the instance where the mRNA translated product, e.g. protein, is vital to the growth of the organism or cellular material, the organism is so transformed or altered such that it becomes, at least, disabled.

Accordingly, in the practices of this invention from a genetic point of view as evidenced by gene expression, new organisms are readily produced. Further, the practices of this invention provide a powerful tool or technique for altering gene expression or organisms through gene therapy. The practices of this invention may cause the organisms to be disabled or incapable of functioning normally or may impart special properties thereto. The DNA of CYP2A6v2 or CYP2A13 employed in the

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practices of this invention can be incorporated into the treated or effected organisms by direct introduction into the nucleus of a eukaryotic organism or by way of a plasmid or suitable vector containing the special DNA of this invention in the case of a procaryotic organism.

BRIEF DESCRIPTION OF THE DRAWINGS

Embodiments of the invention are described by way of example only with reference to the accompanying figures wherein:

Fig. 1. Shows the sequence of exon 2, intron 2 and exon 3 of CYP2C8 and CYP2C9, cDNA sequences (from 4) are shown at the top of the page together with sequences from 6 genomic clones encompassing exon 2, intron 2 and exon 3 of CYP2C8 and CYP2C9. The position of the polymorphism at codon 144 of CYP2C9 and the PCR primers are indicated.

Fig. 2. Shows the sequence of intron 2, exon 3 and intron 3 of CYP2A6, CYP2A7 and CYP2A12. The position of the polymorphism at codon 160 in CYP2A6 and the PCR primers are indicated.

Fig. 3. Shows the detection of CYP2C9 Arg₁₄₄ Cys polymorphism by PCR. Following amplification, samples were digested with AvaII and analyzed on a 1.8 % agarose gel. Lane 1 and lanes 3 to 6 show homozygous wild-type subjects, lane 2 a heterozygous individual and lane 7 undigested PCR product.

Fig. 4. Shows detection of CYP2A6 Leu₁₆₀. His polymorphism by PCR. Two parallel PCR reactions were carried out and the products analyzed on a 1 % agarose gel. Lanes 1, 3, 5 and 7 show the results of the wild-type specific assay and lanes 2, 4, 6 and 8 the results of the variant-specific assay for the same four subjects. Subjects 1 and 2 (lanes 1-4) are homozygous wild-type, subject 3 (lanes 5 and 6) heterozygous and subject 4 (lanes 7 and 8) homozygous for the mutation.

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Fig. 5. Shows distribution of the weekly maintenance doses for warfarin in patients (n=57) homozygous for the CYP2C9 wild-type allele (open bars) and heterozygous (n=37) for the R144C mutant allele (solid bars). Arrows show the median weekly dose requirement of warfarin for each genotype.

Fig. 6. Represents 7-hydroxylation of coumarin (%) in a family genotyped for the CYP2A6 and CYP2A6v1 alleles, showing a subject homozygous for the CYP2A6v1 allele who is deficient in coumarin 7-hydroxylation.

Fig. 7. Shows the difference between the genomic and cDNA sequences for the CYP2A6 gene.

Figs. 8a and b. Shows the conversion event which leads to the CYP2A6v2 allele.

Figs. 9a through 9c. Shows the detection of CYP2A6v2 by PCR. (Fig. 9A) gene-specific amplification by PCR of the CYP2A6 gene using E3F and E3R. Lanes 1 to 4 show the 7.8 Kb band obtained from several representative human genomic DNA templates, lane 5 correspond to a negative control in the absence of template and lane 6 contains 1 Kb DNA ladder (GIBCO BRL) as six markers. (Fig. 9B) Exon-specific PCR amplification of exon 3 from the 7.8 Kb long-PCR product and restriction endonuclease pattern obtained after digestion with *XcmI* (left) and *DdeI* (right) to detect the CYP2A6v1 and CYP2A6v2 alleles, respectively. The genotypes shown correspond to: wild type (+/+), heterozygous (+/-) and homozygous (-/-) subjects. (C) The genotyping strategy which has been developed. Exons are indicated by boxes. The position of the corresponding primer pairs are indicated by horizontal arrows. *XcmI* and *DdeI* restriction sites generate digestion patterns for the different alleles having fragment sizes as shown.

Fig. 10. Schematic diagram depicting methodology underlying a CYP2C9 genotyping assay.

Fig. 11. CYP2A6v2 cDNA sequence.

Fig. 12. CYP2A6v2 genomic DNA sequence having

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7216 base pairs.

Fig. 13. CYP2A13 cDNA sequence.

Fig. 14. CYP2A13 genomic DNA sequence having 8779 base pairs.

Fig. 15. Agarose minigel electrophoresis of PCR products. The CYP2C9 wild-type allele (Arg-144) and R144C respectively, Lanes marked "+/+" and "+/-" contain homozygous wild types and heterozygotes respectively. the right-hand lane contains a 100 bp ladder.

DETAILED DESCRIPTION OF THE INVENTION

The cytochrome P450 isozyme gene, CYP2C9 encodes a high affinity hepatic [S]-warfarin 7-hydroxylase which appears to be principally responsible for the metabolic clearance of the most potent enantiomer of warfarin along with metabolizing a number of other drugs and chemical carcinogens. Similarly, the cytochrome P450 isozyme gene, CYP2A6, encodes a protein that metabolizes nicotine, coumarin and a host of other drugs and chemical carcinogens CYP2A6 also activates the tobacco-specific nitrosamine 4-(methylnitrosamino)-1-(3-pyridyl)-1-butanone (herein referred to as "NNK"). Many cancers have been associated with activation and/or accumulation of nitrosamines. The present invention allows detection of a predisposition to such cancers.

It is of note that the above gene products are also known to metabolize other substrates. For example, the CYP2C9 gene product is also known to metabolize Tolbutamide, Phenytoin, Ibuprofen, Imipramine, Naproxen, Tienilic acid, Diclofenac and Tetrahydrocannabinol and hence can also be used to detect sensitivities to these drugs. A list of CYP2C9 drug substrates has been documented and is incorporated herein by reference (Gonzalez & Idle 1994 *Clin. Pharmacokinet* 26:59-70). Hence, the present invention can be used to screen for sensitivities to these drugs.

In addition, CYP2C9 has been associated with the metabolism of chemical carcinogens; such as polycyclic

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aromatic hydrocarbons. For example, the most ubiquitous environmental carcinogen, benz-[a]-pyrene is metabolized by CYP2C9. Benz-[a]-pyrene is found in tobacco, barbecued meats, car exhaust and generally, in polluted air. This compound, as it accumulates in the body becomes a potent DNA intercalating agent, ultimately resulting in cell transformation and the formation of tumors. The present invention provides a diagnostic method of screening individuals for their ability to metabolize and hence inactivate benz-[a]-pyrene. For example, a homozygote wild-type CYP2C9 individual would be better able to tolerate high levels of benz-[a]-pyrene than a heterozygote of the CYP2C9 allele.

Similarly, the CYP2A6 allele is associated with drug sensitivity and carcinogen metabolism. Coumarin sensitivity is directly related to the presence of a variant CYP2A6 allele, such as CYP2A6v1, CYP2A6v2 and also CYP2A13. Coumarin is a drug used in treatment of neoplastic diseases, such as lymphomas. (See Martindale: The Extra Pharmacopoeia 1993 Ed. Reynolds, J.E.F., The Pharmaceutical Press, London, p. 1358). Its suggested dosage is very high. Therefore, the present invention is useful in determining a patient's sensitivity to the drug in order to prescribe a proper dosage and avoid toxicity.

Another drug, Thiotepa[™], is used in the treatment of a variety of neoplastic diseases, such as in treating women with breast cancer and children with brain tumors. Thiotepa is metabolized by CYP2A6 into Tepa, which is an intermediate more therapeutically potent than Thiotepa. Therefore, if a patient has a very active CYP2A6 enzyme, it is likely the patient will require lower doses of Thiotepa to provide a therapeutically effective amount. As one can see, the dosage provided to a patient is dependent upon the rate a patient is capable of metabolizing activating the drug. The present invention has identified variant alleles whose enzymatic activity is compromised. In addition, the present invention provides

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° a simple method of genotyping patients for Thiotepa drug sensitivity. With information concerning patient sensitivity to such drugs, the proper dosage can be provided, hence maximizing drug efficiency and minimizing drug toxicity.

5 Further, CYP2A6 has been associated with nicotine metabolism. In addition to being an active ingredient in tobacco, nicotine also has several clinical uses. Nicotine is used clinically to treat various neurological disorders, such as Parkinson's disease and
10 Alzheimer's disease. In addition, nicotine is used to treat tobacco addiction. In all of these situations, it is important to know a patient's sensitivity to nicotine, since extremely sensitive patients will become violently ill upon administration of nicotine. Therefore the
15 present invention provides a method of identifying nicotine-sensitive patients by genotyping a patient's CYP2A6 allele. The present invention also provides a convenient method for determining an individual's general predisposition to using tobacco based upon their
20 sensitivity to nicotine.

In addition, CYP2A6 is involved in activating nitrosamines, thereby producing the potent carcinogen NNK. Increased levels of NNK have been associated with a variety of cancers, including but not limited to lung
25 cancer, nasal-pharynx cancers, throat cancers and colon cancers. In general, elevated levels of CYP2A6 has been associated with cancers associated with exposure to nitrosamines. The present invention may detect a patient's predisposition to such cancers. The presence of
30 a CYP2A6 gene or a variant thereof will affect the likelihood that procarcinogens present in tobacco smoke will be activated into carcinogenic nitrosamines and nitrosamine-derivatives and therefore result in the development of a cancer.

35 It follows that genetic polymorphisms or mutations in either of the two aforementioned genes can

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lead to an impairment in metabolism of at least the aforementioned drugs and chemical carcinogens.

The present invention relates to the identification of the absence or presence of mutations in CYP2C9 and CYP2A6 and thus predict the phenotype of an individual and so predict whether and how an individual is likely to metabolize particular drugs and chemical carcinogens. For instance, the R144C mutation arising from a C₄₇₂→T base substitution in the CYP2C9 gene results in a reduction in warfarin metabolism. This implies that patients with this mutation receiving warfarin require a lower dose to maintain an anticoagulation target than those patients who do not have the mutation and are also receiving warfarin. Conversely, homozygous wild-types require higher doses in order to maintain an anticoagulation target.

"Mutation", as the term is used herein denotes an allelic variation of a known sequence, which alters the expressed gene product's activity. Such a variation need not completely inactivate the gene product's activity but merely alter it.

Similarly, one mutation within CYP2A6v1 arising from a T₄₈₈→A base change results in substitution of Leucine 160 by Histidine. Another CYP2A6 variant, CYP2A6v2, has been identified which differs from CYP2A6 in the regions of exons 3, 6 and 8. One particular mutation in CYP2A6v2, T₄₁₅→A mutation is useful in the assay of the present invention. These substitutions are very useful in detecting predispositions to cancers associated with tobacco and activation of nitrosamines. The normal CYP2A6 enzyme functions in the metabolism of nicotine, one of the carcinogenic compounds in tobacco.

In addition, the present invention relates to the identification of a new variant of CYP2A6 designated CYP2A6v2. The variations of CYP2A6v2 from CYP2A6 bear sequence relatedness with the corresponding exons of the CYP2A7 gene, suggesting a recent gene conversion. The cDNA

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and genomic sequence for this gene is provided in the present invention. Hence, at least three different allelic variants of CYP2A6 exist and are illustrated in Figure 8. These allelic variants include CYP2A6, CYP2A6v1 and CYP2A6v2.

Further, the present invention relates to a new CYP2A gene, designated CYP2A13. This gene produces an inactive form of CYP2A6, however variants at particular positions, including amino acid positions 117, 209 and 365 produce an enzyme which may alter the enzyme's activity and hence affect drug sensitivity. These mutations in CYP2A6 are likely to result in a deficiency or impaired activity of one of the enzymes responsible, for example, for metabolizing drugs, nicotine and nitrosamines.

CYP2A13 is considered a new cytochrome P450 gene. However, since the CYP2A13 gene product has a similar function as the CYP2A6, it is discussed herein as a variant of CYP2A6. That is, assays using the specific mutated amino acid positions 117, 209 and 365 of CYP2A13 and detecting variations at those positions are indicative of CYP2A6-like variant functions.

In one embodiment, the CYP2A6v2 or CYP2A13 proteins or functional portions thereof are expressed as recombinant genes in a cell, so that the cells may be transplanted into an individual in need of gene therapy due to the predisposition to a carcinogen-associated cancer or a sensitivity to a drug. To provide gene therapy to an individual, a genetic sequence which encodes for all or part of the CYP2A6v2 or CYP2A13 ligands are inserted into vectors and introduced into host cells. Examples of vectors that may be used in gene therapy include, but are not limited to, defective retroviral, adenoviral, or other viral vectors (see, e.g., Mulligan, R.C., 1993, Science, 260:926-932). The means by which the vector carrying the gene may be introduced into the cell includes, but is not limited to, microinjection, electroporation, transduction, or transfection using DEAE-

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dextran, lipofection, calcium phosphate or other procedures known to the skilled routineer (see, e.g., Sambrook et. al. (Eds.), 1989, In "Molecular Cloning. A Laboratory Manual", Cold Spring Harbor Press, Plainview, New York). Examples of cells into which the vector carrying the gene may be introduced include, but are not limited to, continuous culture cells, such as COS, NIH/3T3, and primary or culture cells of the relevant tissue type.

More specifically, there is provided a method of enhancing the therapeutic effects of blood cells, that are infused in a patient, comprising: (i) inserting into the blood cells of a patient a DNA (RNA) segment encoding CYP2A6v2 or CYP2A13 gene product that enhances the therapeutic effects of the blood cells; and (ii) introducing cells resulting from step (i) into the patient under conditions such that the cells resulting from step (i) "target" to a tissue site. In the alternative, as previously described the cells are not "targeted" and functions as a systemic therapeutic. The genes are inserted in such a manner that the patient's transformed blood cell will produce the agent in the patient's body. In the case of antigen-specific blood cells which are specific for an antigen present at the tissue site, the specificity of the blood cells for the antigen is not lost when the cell produces the product.

Alternatively, as hereinabove indicated, CYP2A6v2 or CYP2A13 DNA (RNA) may be inserted into the blood cells of a patient, in vivo, by administering such DNA (RNA) in a vehicle which targets such blood cells.

Further details regarding methods of gene therapy are provided in Anderson et al., U.S. Patent No. 5,399,343 which is herewith incorporated herein by reference.

In another embodiment, antisense CYP2A6v2 or CYP2A13 DNA or RNA may be used to control the expression of CYP2 gene. For example, antisense therapy may be used

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to control CYP2A6's ability to activate dangerous nitrosamines by curbing its expression. Methods of producing such antisense molecules are described in U.S. Patent No. 5,190,931, which is incorporated herein by reference.

Developing a genotyping assay, which could distinguish the CYP2 genes of interest from other cytochrome P450 genes required careful engineering since these genes have a high degree of sequence homology. To overcome this problem, one embodiment of the present invention has elucidated the genomic sequence structure of CYP2C9 and CYP2A6 with a view to making, in part, intron specific primers. That is to say primers which, in part, hybridize to at least one intron, preferably an intron adjacent to an exon including the mutation of interest, in the gene to be examined. Since there is less homology between the introns of cytochrome P450 genes, it has been found that using intron specific primers, gene specific assay can be undertaken. The present invention has a further advantage of using intron specific primers in so far as the use of such primers facilitates the manufacture of an optimum length of DNA which in turn facilitates the specificity of the instant bioassay.

A "genotyping" assay as the term is used herein refers to any diagnostic or predictive test to detect the presence or absence of allelic variants of a known gene sequence at a specified gene locus. Two gene loci are of particular interest in the present invention, CYP2A6 and CYP2C9.

Further, the present invention relates to differences between the genomic DNA sequence structure and the cDNA sequence structure, as illustrated in Figure 7. As a result, primers directed at the genomic sequence structure have been developed which are more reliable.

Several methods are provided for identifying the presence or absence of a mutation at codon 144 of the coding sequence of CYP2C9, or alternatively, at codon 160

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of the coding sequence of CYP2A6, or alternatively, a gene conversion event involving CYP2A6 and CYP2A7 in exons 3, 6 or 8 comprising a DNA encompassing the region of a CYP2 gene unique to that variant.

One such method relates to an assay which contemplates the use of one specific primer which specifically encompasses the region containing the mutation, and a second primer which is complementary to another portion of the gene. The second primer sequence chosen is based upon the CYP2A6, CYP2C9 or CYP2A13 sequences as set forth in figures 12, 1 and 14, respectively, depending upon the preferred size of the amplification product. One skilled in the art will know how to select second primer based on the region of gene chosen for amplification. These primers need not be identical to a given sequence but must be sufficiently complementary to hybridize to the target region in a specific manner. In short, the primers are preferably at least substantially homologous to the nucleic acid sequence provided.

Nucleic acid sequences includes, but is not limited to, DNA, RNA or cDNA. Nucleic acid sequence as used herein refers to an isolated nucleic acid sequence. Substantially homologous as used herein refers to substantial correspondence between the nucleic acid primer sequence of as described herein and that of any other nucleic acid sequence. Substantially homologous means about 50-100% homologous homology, preferably by about 70-100% homology, and most preferably about 90-100% homology between the particular sequence discussed and that of any other nucleic acid sequence.

In the instant application, the term "primer" is further used to designate a molecule comprising at least three nucleotides, the exact length being determined by the requisite amount of DNA needed, under given reaction conditions, to bind to or interact with a test sample so as to identify the presence or absence of either of said

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mutations. Preferably, the primer is usually between 15 and ideally about 20 to 50 oligonucleotides in length.

The primer is selected, or adapted, to be substantially complementary to a part of DNA which is adjacent to the region of at least one of the
5 aforementioned mutations. Thus such a primer is able to hybridize with a part of DNA that contains a region in which the mutation of interest may be found. Although the primer may not reflect the exact sequence of the region in which the mutation is thought to occur, the more closely
10 the primer is to this sequence, then the better the binding will be. Ideally, the more closely the sequence of the 3' end of the primer is to said region the better the binding or interaction will be.

An alternative method for using the sequence
15 unique to a variant for detection relates to use of an oligonucleotide probe for specifically detecting the presence or absence of a CYP2 variant gene in a sample. this method comprises the steps of contacting the sample with a nucleic acid probe, allowing hybridization, forming
20 a probe: CYP2 variant complex; washing excess probe from probe: CYP2 variant complex; and detecting probe: CYP2 variant complex, wherein a positive signal is an indication of the presence of the CYP2 variant in the sample.

25 The hybridization of the probe to sample nucleic acids can be carried out by any of the methods commonly used in the art. Such methods include but are not limited to, Dot blot, Colony hybridization, Southern blot, solution hybridization and *in situ* hybridization.

30 Washing the excess probe from the probe: CYP2 variant DNA can be accomplished by many well-known methods. Simply rinsing the complex with excess buffer will facilitate removal of excess probe. Alternatively, washing may entail separating the probe: CYP2 variant
35 complex from excess probe. Many methods are known to one skilled in the art and include but are not limited to

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centrifugation, filtration and magnetic force.

According to the present invention there is provided a portion of DNA suitable for use as a primer in a method for identifying the presence or absence of a mutation either at codon 144 of the coding sequence of the gene CYP2C9, or alternatively, at least one gene conversion event involving CYP2A6 and CYP2A7 in exons 3, 6 or 8, or alternatively, at codon 160 of the coding sequence of the gene CYP2A6; comprising a DNA which is adapted to hybridize to at least one intron of at least one of said genes.

In one embodiment, the method comprises the use of at least one restriction endonuclease to digest DNA from individuals to be tested. In this instance, DNA from individuals positive for the wild-type form of CYP2C9 provide a digest with a restriction endonuclease, such as *Ava*II results in production of two fragments, a first fragment including 270 base pairs and a second fragment including 50 base pairs. In contrast, individuals having the aforementioned mutation in CYP2C9 present a single fragment of 320 base pairs only. This is due to a loss of the *Ava*II site. The CYP2A6 gene variants can also be distinguished by the occurrence of specific restriction endonuclease sites. The CYP2A6v1 variant, which is a T₄₈₈→A mutation in exon 3 can be identified by a variant-specific *Xcm*I restriction site. The CYP2A6v2 variant, which contains a C₄₁₅→A mutation within exon 3 can be identified by a variant-specific *Dde*I restriction site. The wild-type CYP2A6 gene does not contain either an *Xcm*I or *Dde*I site. The results of such restriction endonuclease digestions are illustrated in Figure 9.

It may be necessary to amplify the DNA prior to digestion. Such may be the case when the DNA of interest is present in minute quantities in a sample. In such circumstances, amplification of DNA to be tested is undertaken before digesting the DNA as described above. This provides for a greater quantity of materials.

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Amplification is performed using any conventional technique, such as by a PCR reaction. Many other techniques for amplification can be used in producing sufficient DNA for detections. Such amplification techniques are well-known to the skilled artisan and include, but are not limited to polymerase chain reaction (PCR), PCR *in situ*, ligase amplification reaction (LAR), ligase hybridization, QB bacteriophage replicase, transcription-based amplification system (TAS), genomic amplification with transcript sequencing (GAWTS) and nucleic acid sequence-based amplification (NASBA). A general review of these methods is available in Landegren, et al., *Science* 242:229-237 (1988) and Lewis, R., *Genetic Engineering News* 10:1, 54-55 (1990), which is incorporated herein by reference.

One embodiment of the present invention uses oligonucleotide primers in an amplification and detection assay. A basic description of nucleic acid amplification is described in Mullis, U.S. Patent No. 4,683,202, which is incorporated herein by reference. The amplification reaction uses a template nucleic acid contained in a sample, two primer sequences and inducing agents. The extension product of one primer when hybridized to the second primer becomes a template for the production of a complementary extension product and vice versa, and the process is repeated as often as is necessary to produce a detectable amount of the sequence.

The inducing agent may be any compound or system which will function to accomplish the synthesis of primer extension products, including enzymes. Suitable enzymes for this purpose include, for example, *E.coli* DNA polymerase I, thermostable *Taq* DNA polymerase, Klenow fragment of *E.coli* DNA polymerase I, T4 DNA polymerase, other available DNA polymerases, reverse transcriptase and other enzymes which will facilitate combination of the nucleotides in the proper manner to form amplification products.

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A sample being screened for the presence or absence of a mutation in CYP2A6 and/or CYP2C9 genes can be tested with the instant invention. The nucleic acid material can be in purified or nonpurified form, provided the sample contains the CYP2A6 and/or CYP2C9 genes. The sample may be derived from any tissue or bodily fluid, wherein the patient's DNA can be found. A clinically practical type of sample is a blood specimen which contains patient DNA and can conveniently be genotyped in the bioassay of the present invention.

The "primers", as the term is used in the present invention refers to an oligonucleotide, whether occurring naturally as in a purified restriction digest or produced synthetically, which is capable of acting as a point of initiation of synthesis when placed under conditions wherein synthesis of a primer extension product which is complementary to a nucleic acid strand is induced, i.e. in the presence of nucleotides and an inducing agent such as DNA polymerase and at a suitable temperature and pH. The primers are preferably single stranded for maximum efficiency in amplification, but may alternatively be double stranded. If double stranded, the primer is first treated to separate its strands before being used to prepare amplification products. Preferably, the primers are oligodeoxyribonucleotides. The primers must be sufficiently long to prime the synthesis of extension products in the presence of the inducing agent. The exact lengths of the primers will depend on many factors, including temperature, source of primer and use of the method. For diagnostic methods, the primers typically contain at least 10 or more nucleotides. The oligonucleotide primers may be prepared using any suitable method, such as, for example, the phosphotriester and phosphodiester methods (Narang, S.A., et al., *Meth. Enzymol.* 68:90 (1979); Brown E.L., et al., *Meth. Enzymol.*, 68:109 (1979)) or automated embodiments thereof. In one such automated embodiment diethylphosphoramidites are used

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as starting materials and may be synthesized as described by Beaucage et al., *Tetrahedron Letters* 22:1859-1962 (1981). One method for synthesizing oligonucleotides on a modified solid support is described in U.S. Pat. No. 4,458,066. It is also possible to use a primer which has been isolated from a biological source (such as a restriction endonuclease digest).

In a genotyping bioassay of the present invention, one embodiment comprises a gene-specific amplification reaction, an exon-specific amplification reaction and a restriction endonuclease reaction. In such a reaction a suitable polynucleotide polymerase is used in the amplification reaction, many of which have already been described in the art. In addition, any appropriate restriction endonuclease which is designed to digest the DNA and so provide information concerning genotype may be used.

It may further be necessary to provide a label on the nucleic acid for detection. The nucleic acid can be DNA or RNA and made detectable by any of the many labeling techniques readily available and known to the skilled artisan. Such methods include, but are not limited to, radio-labelling, digoxigenin-labeling, and biotin-labeling. A well-known method of labeling DNA is ^{32}P using DNA polymerase, Klenow enzyme or polynucleotide kinase. In addition, there are known non-radioactive techniques for signal amplification including methods for attaching chemical moieties to pyrimidine and purine rings (Dale, R.N.K. et al. 1973 *Proc. Natl. Acad. Sci. USA*, 70:2238-2242; Heck, R.F. 1968 *S. Am. Chem. Soc.*, 90:5518-5523), methods which allow detection by chemiluminescence (Barton, S.K. et al. 1992 *J. Am. Chem. Soc.*, 114:8736-8740) and methods utilizing biotinylated nucleic acid probes (Johnson, T.K. et al. 1983 *Anal. Biochem.*, 133:125-131; Erickson, P.F. et al. 1982 *J. of Immunology Methods*, 51:241-249; Matthaei, F.S. et al 1986 *Anal. Biochem.*, 157:123-128) and methods which allow detection by

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fluorescence using commercially available products. Non-radioactive labelling kits are also commercially available. Such a label can readily be incorporated into the nucleic acid during an amplification step. In the absence of an amplification step, a target nucleic acid can readily be chemically or enzymatically modified to carry a label. Additionally, it may be preferable to provide a labeled primer which may serve to incorporate a label into the nucleic acid target. Probes, as may be used in an embodiment of the invention may also be chemically or enzymatically labeled as described above.

In a preferred embodiment of the invention said DNA primer hybridizes to an intron adjacent said position of said mutation. Preferably said DNA is a primer with the 3'-end specific for the gene of interest. Preferably further still said DNA is single stranded. Preferably further still, in so far as the CYP2C9 mutation is concerned, said primers are as follows:

HF18: position 8 of intron 2 onwards of genomic sequence in forward orientation comprises
5' TGCAAGTGCCTGTTTCAGCA 3'
HF2R: position 505 onwards of cDNA sequence in reverse orientation comprises
5' AGCCTTGGTTTTTCTCAACTC 3'.

It is of note that both these primers are designed to be specific for CYP2C9 and so do not amplify related genes such as CYP2C8, which notably also has an Arginine₁₄₄ present.

Preferably, in so far as CYP2A6 is concerned, three primers J51, J61 and B are used in two parallel allele-specific PCR reactions. These primers are as follows:

J51 comprises 5' GGCTTCCTCATCGACGCACT 3'
(forward strand from position 479 of cDNA

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sequence described as hIIA3 (Yamano, et al. 1990 *Biochem* 29:1322-29)).

J61 comprises 5' GGCTTCCTCATCGACGCACA 3' (forward strand from position 479 of cDNA sequence described as hIIA3v (Yamano, et al. 1990 *Biochem* 29:1322-29)).

Both J51 and J61 contain a substitution at position 18 of A for C to give improved specificity as suggested by Newton et al (1989 *Nuc. Acids Res.* 17:2503-2516).

Primer B comprises 5' AATTCAGGAGGCAGGGCCT 3' (reverse orientation from position 125 of intron 3 of CYP2A6 (onwards). Designed so that only CYP2A6 and not CYP2A7 or CYP2A12 are amplified.

One method of genotyping CYP2A6 provides an allele-specific amplification reaction method is used. In this instance, DNA which is adapted to specifically hybridize to the wild-type or the mutant type of the gene is incubated with test DNA under reaction conditions and the resultant products are analyzed by electrophoresis and then visualized by staining with ethidium bromide. Individuals who are homozygous for the wild-type allele produce a reaction product with primer J51 only. Similarly, individuals who are homozygous for the mutation produce a reaction product with primer J61 only. Those individuals who are heterozygous produce a reaction product with both J51 and J61.

Alternatively, another method for genotyping CYP2A6 is provided in a specific amplification bioassay, which is achieved with primers F4 and R4 as follows:

The F4 primer (forward) comprises 5' CCCCTTATCCTCCCTTGCTGGCTGTGTCCCAAGCTAGGCAGGATT CATGGTGGGGCA 3', wherein a preferred fragment thereof further comprises 5' CCTCCCTTGCTGGCTGTGTCCCAAGCTAGGC 3'.

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The R4 primer (reverse) comprises

5' GCCACCACGCCCCCTTCCTTTCCGCCATCCTGCCCCCAGTCTTAGC
TGCGCCCCCTCTC 3', wherein a preferred fragment
thereof further comprises
5' CGCCCCTTCCTTTCCGCCATCCTGCCCCCAG 3'.

This method of CYP2A6 genotyping involves a first amplification reaction with F4 and R4 primers, which generates a DNA fragment approximately 7.8 kb in size. This amplification step is facilitated by polymerases which are capable of transcribing long stretches of DNA. To distinguish the CYP26Av1 and CYP26Av2 variant alleles, an exon-specific amplification step is carried out using the 7.8 Kb DNA fragment as template DNA. This may be accomplished using the following primer pair:

The E3F primer (forward) comprises

5' CCTGATCGACTAGGCGTGGTATTTCAGCAACGGGGAGCGCGCCAAG
CAGCTCCTG 3', wherein a preferred fragment
thereof further comprises
5' GCGTGGTATTTCAGCAACGGG 3'.

The E3R primer (reverse) comprises

5' CGCGCGGGTTCCTCGTCCTGGGTGTTTTCCTTCTCCTGCCCCCGC
ACTCGGGATGCG 3', wherein a preferred fragment
thereof further comprises
5' TCGTCCTGGGTGTTTTCCTTC 3'.

Using these primers in a second amplification reaction step a segment of CYP2A6 exon 3 is specifically amplified. The method further comprises use of the restriction endonuclease *XcmI* to detect the CYP2A6v1 mutation and *DdeI* to detect the CYP2A6v2 mutation.

According to a yet further aspect of the invention there is provided a kit for performing the afore described methods which kit includes at least a portion of DNA in accordance with the invention and preferably at least one control sample of DNA containing the mutation or

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mutations of interest and ideally also a wild-type sample of DNA so that suitable comparisons can be made.

It is of note that although the method is described with reference to the above methods, any suitable method using the genetic material of the invention may be used to identify the mutations described herein.

The CYP2C9 assay has been used in a study of warfarin dose requirement in 94 patients undergoing anticoagulant treatment and the results obtained are summarized in Figure 5. 58 patients (61.7%) were homozygous for the wild-type (Arg₁₄₄) allele and were found to require a median weekly maintenance dose of 31.5 mg of warfarin. 36 patients (38.6%) were heterozygous and required a median weekly maintenance dose of 24.5 mg. The doses required by the two groups were significantly different (Mann-Whitney U-test, $p = 0.016$). No subjects in the group were homozygous for the mutant allele but based on allele frequencies and the Hardy Weinberg equilibrium, the predicted frequency of homozygous mutant subjects is 3.7%.

Comparison of the weekly maintenance dose of warfarin in the R144C heterozygotes ($n = 36$) and homozygous wild-type ($n = 58$) reveals that the heterozygotes required a significantly lower dose (range of 10.5 - 80.0 mg). Moreover, of the patients requiring the lowest doses to maintain an anticoagulation target (INR 2.0-4.0), in the range 5-15 mg per week, 9 out of 10 were heterozygous. At the other extreme of weekly doses >55 mg, 5 out of 6 patients were homozygous wild-type for CYP2C9. The significantly lower (20%) warfarin dose requirement of the patients with one variant R144C allele is consistent with the kinetic properties of the R144C protein with respect to (S)-warfarin hydroxylation and presumed *in vivo* metabolic clearance (Rettie et al. 1994 *Pharmacogen.*, 4:39-42).

The CYP2A6 genotyping assay has been used in

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studies on coumarin metabolism. Coumarin 7-hydroxylase activity is a convenient marker activity to identify the presence of CYP2A6 in a particular sample. There is considerable variation in the ability of individuals to 7-hydroxylate this compound which is a reaction specific for CYP2A6. A subject deficient in coumarin 7-hydroxylation has been identified. This subject is homozygous for the mutant CYP2A6v1 allele confirming the previous *in vitro* findings that substitution of Leu160 by His results in loss of coumarin 7-hydroxylase activity. As shown in Fig. 6, CYP2A6 genotyping and phenotyping with coumarin has been performed on other members of the proband's family and impaired coumarin 7-hydroxylation has been observed in heterozygotes for the CYP2A6v1 mutation.

The genotyping assays described herein resulted from a two step amplification reaction wherein first amplification reaction amplifies a 7.8 Kb fragment containing the CYP2A6 gene (Fig. 9A) and a second amplification reaction amplifies an exon-specific fragment of CYP2A6. The amplification product was digested with restriction endonucleases producing different patterns for the various CYP2A6 alleles. Representative results obtained for several human subjects for the detection of the CYP2A6v1 (*XcmI* digestion) and CYP2A6v2 (*DdeI* digestion) are shown in Figure 9 panel B. A schematic depiction of this genotyping assay is shown in Figure 9, panel C. Of 155 human genomic DNA samples analyzed 21 heterozygous (+/-) and 6 homozygous (-/-) subjects were detected for the CYP2A6v1 allele, whereas 17 heterozygous (+/-) and no homozygous were identified for the CYP2A6v2 allele variant. Additionally, 7 homozygous for both CYP2A6v1 and CYP2A6v2 alleles were found.

Allelic frequencies were calculated for either allele in several ethnic groups and analyzed as shown in Table 1. CYP2A6v1 frequency is almost identical between Caucasian and Japanese, and it is only twice the frequency in Taiwanese samples. Significantly, this allele is

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completely absent in the African-American population within the samples studied. The Japanese population has a remarkable higher frequency for the CYP2A6v2 allele (28%) as compared to the Caucasian (2%), Taiwanese (6%) or African-American (2.5%) (ethnic groups).

Table 1: Allelic frequency for the CYP2A6 gene in different ethnic groups.

Ethnic Group	Allelic Frequencies (%)			
	CYP2A6	CYP2A6v1	CYP2A6v2	N
Caucasian	75	23	2	52
Japanese	52	20	28	40
Taiwanese	83	11	6	178
African-American	97.5	0	2.5	40

The following examples illustrate various aspects of the present invention and in no way are intended to limit the scope thereof. All books, articles, and patents referenced herein are incorporated herein, in toto, by reference. Other similar embodiments will be clear to the skilled artisan and are encompassed within the spirit and purview of the present invention.

EXAMPLE 1

Method for determining the genotype CYP2C9

Genotyping for the CYP2C9 polymorphism is carried out by amplification by PCR followed by digestion with the restriction endonuclease AvaII. Amplifications are performed in 0.5 ml microcentrifuge tubes in a volume of 100 μ l containing 10 mM Tris-HCl, pH 8.8, 1.5 mM MgCl₂, 50 mM KCl, 0.1% Triton X-100, 5% dimethylsulphoxide, 200 μ M each of dTTP, dATP, dCTP and dGTP, 250 μ M of the primers HF18 and HF2R, 2.5 units Taq polymerase and 1 μ g human leukocyte genomic DNA. PCR conditions consist of 35 cycles with a denaturation at 93°C for 1 min. annealing at 55°C for 1.5 min and polymerization at 72°C for 1 min. 20 μ l of the amplified DNA is incubated with 10 units AvaII for 3h at 37°C and then analyzed by electrophoresis on

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1.8% agarose minigels in TBE (90 mM Tris-borate, 2 mM EDTA) buffer. The digestion products are visualized by ethidium bromide staining. DNA from individuals positive for the wild-type Arg₁₄₄ is digested to give fragments of 270 bp and 50 bp whereas in individuals with the mutant Cys₁₄₄ present, a band of 320 bp is seen due to loss of an AvaII site (Figure 3).

EXAMPLE 2

Genotyping for the CYP2C9 polymorphism was carried out by amplification by PCR followed by digestion with the restriction endonuclease AvaII.

One hundred patients were recruited from two anticoagulation clinics in the Newcastle area over four study days. Body weight and height were measured, the basal metabolic index ("BMI") calculated for each patient and details of age, sex, drug history, current and previous International Normalized Ratio ("INR") determinations, indications for anticoagulation and other significant health problems were all recorded. DNA was isolated by a standard manual chloroform-phenol extraction procedure and 1µg was subjected to PCR analysis. As shown in Figure 10 the C-T substitution, which converts Arg-144 to Cys, resides in exon 3 of the CYP2C9 gene and results in the loss of an AvaII restriction site (...GAGGACCGTGTTCAA...) in the R144C allele (...GAGGACTGTGTTCAA...). This provided the basis of the amplification strategy. A CYP2C9 specific intron forward primer (HF18, TGCAAGTGCCTGTTTCAGCA, Figure 10) and a CYP2C9 exon 3 3'-end reverse primer (HF2R, AGCCTTGTTTTTCTCAACTC, Figure 10) were used at a concentration of 250µM each. Amplifications were performed in a volume of 100 µl containing 20 mM Tris HCl (pH 8.3), 1.5 mM MgCl₂, 25 mM KCl, 0.05% (w/v) Tween 20, 10 µg gelatin/ml, 2% (w/v) DMSO, 200 µM each of dATP, dCTP, dGTP and dTTP and 2.5 units of Taq DNA polymerase (Perkin-Elmer). Reactions were carried out for 35 cycles

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at an annealing temperature of 55°C for 90 sec, a polymerase temperature of 72°C for 1 min, and a heat denaturing temperature of 93°C for 1 min, using a Perkin-Elmer Cetus DNA thermal cycler. The PCR products digested with AvaII and sized using NuSieve agarose gels (3% NuSieve, 0.75% agarose). Presence of the CYP2C9 wild-type and R144C alleles were detected as fragments of 50 + 270 bp and 320 bp respectively (see Figures 3). The PCR product synthesized from human genomic DNA with the primers HF18/HF2R was directly sequenced on an ABI 373A automatic sequencer. Briefly, the PCR product was first purified by using the Wizard DNA clean-up system (Promega Co., Madison, WI). The purified template was then subjected to dideoxy terminator cycle-sequencing with the primers HF18 and HF2R. The primer-extended products were purified and sequenced following the manufacturer's procedure. Sequence analysis was done by using the MacVector software program (Eastman-Kodak Co., Rochester, NY).

DNA was obtained from 94 patients. Of these 58 (62%) were homozygous for the wild-type CYP2C9 gene and 36 (38%) were heterozygous for the R144C allele. No R144C homozygotes were found. The frequency of the wild-type (Arg-144) and R144C (Cys-144) alleles in the study population is thus 0.808 and 0.192 respectively. An expectation of 3.7% R144C homozygotes can be anticipated from the Hardy-Weinberg equilibrium, but the 95% confidence interval in this estimation of 0.8-8.4% and thus the finding of zero homozygotes in 94 patients is not significantly different from expectation. The specificity of the PCR reaction with respect to the CYP2C9 gene was confirmed by sequencing. The alignment of the sequence obtained from the PCR product with that corresponding to the CYP2C9 gene showed a 100% degree of homology. Interestingly, a heterozygous pattern was obtained for the R144C allelic variant, confirming the high frequency of this allele within the normal population. No sequence

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deriving from CYP2C9, CYP2C18 or CYP2C19 was found confirming the specificity of the assay for CYP2C9.

EXAMPLE 3

Method for determining the genotype CYP2A6

Genotyping for the CYP2A6 polymorphism is carried out by allele-specific PCR using two parallel PCR reactions, one specific for the wild-type allele, one for the mutant allele. Amplifications are performed in 0.5 ml microcentrifuge tubes in a volume of 45 μ l containing 10 mM Tris-HCl, pH 8.8, 1.5 mM MgCl₂, 50 mM KCl, 0.1 % Triton X-100, 5 % dimethylsulfoxide, 200 μ M each of dTTP, dATP, dCTP and dGTP, 250 μ M of the primers B and either J51 or J61, 1.25 units Taq polymerase and 1 μ g human leukocyte genomic DNA. PCR conditions consist of 40 cycles with a denaturation at 93°C for 1 min., annealing at 57°C for 2 min and polymerization at 70°C for 2 min. The products are analyzed by electrophoresis on 1% agarose minigels in TBE buffer and DNA is visualized by staining with ethidium bromide. As shown in Figure 4, there are three possible results: the individual may be homozygous for the wild-type allele and give a DNA product only for the PCR reaction with primer J51, the individual may be heterozygous with one wild-type and one mutant allele and give DNA products with both primers J51 and J61 or the individual may be homozygous for the mutation and give a DNA product only with the J61 primer.

EXAMPLE 4

Alternative Method for Determining the Genotype CYP2A6

For use of F4 and R4 primers, each reaction mixture contained 600 ng human genomic DNA, 0.2 μ M of each primer, 200 μ M dNTP's, 0.8 mM magnesium acetate and 2 units of rTth I DNA polymerase. Hot start was as indicated by the manufacturer (Perkin Elmer) and the amplification reaction of 31 cycles of 93°C, 1 min; 66°C, 6 min 30 sec. Amplification products were analyzed in

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0.7% agarose gels and the DNA visualized by staining with ethidium bromide. For the exon 3 specific amplification, the reaction which uses, the primers E3F and E3R consist of 5 μ l of the 7.8 Kb PCR reaction, 0.5 μ M of each primer, 200 μ M dNTP's, 1.5 mM MgCl₂ and 2.5 units of Taq DNA polymerase. The amplification reaction consisted of 94°C for 3 minutes followed by 31 cycles of 94°C, 1 minute; 60°C, 1 minute and 72°C, 1 minute.

Amplification products were then digested without purification with restriction endonucleases which detect the CYP2A6 wild type (no digestion), CYP2A6v1 (XcmI) and CYP2A6v2 (DdeI). DNA was visualized by use of ethidium bromide after electrophoresis in 1% agarose, 3% NuSieve agarose.

It is of note that CYP2C9 genotyping can be performed using an allele-specific assay similar to that used above for CYP2A6.

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CLAIMS

1. A CYP2A6v2 DNA having a coding sequence shown in Figure 11.

5 2. The DNA of claim 1 having a genomic sequence as shown in Figure 12.

10 3. A CYP2A13 DNA having a coding sequence shown in Figure 13.

4. The DNA of claim 3 having a genomic sequence shown in Figure 14.

15 5. A nucleic acid primer sequence comprising at least ten (10) contiguous nucleotide bases selected from the sequence showing in Figure 12.

20 6. A nucleic acid primer sequence comprising at least ten (10) contiguous nucleotide bases selected from the sequence shown in Figure 14.

7. A nucleic acid primer sequence selected from the group consisting of:

- 25 A. 5' GGCTTCCTCATCGACGCACT 3';
B. 5' GGCTTCCTCATCGACGCACA 3';
C. 5' AATTCCAGGAGGCAGGGCCT 3';
D. 5' TGCAAGTGCCTGTTTCAGCA 3';
E. 5' AGCCTTGGTTTTTCTCAACTC 3';
F. 5' CCCCTTATCCTCCCTTGCTGGCTGTGTCCCAAGCTAGGCA
30 GGATTCATGGTGGGGCA 3';
G. 5' GCCACCACGCCCCTTCCTTTCGCCATCCTGCCCCCAGTC
TTAGCTGCGCCCCTCTC 3';
H. 5' CCTGATCGACTAGGCGTGGTATTCAGCAACGGGGAGCGCG
CCAAGCAGCTCCTG 3';
35 I. 5' CGCGCGGGTTCCTCGTCCTGGGTGTTTTCTTCTCCTGCC
CCCGCACTCGGGATGCG 3';

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°
or any nucleic acid sequence of at least 10 contiguous nucleotides selected from any one of A-I.

5 8. A method of determining the presence or absence of an allelic variant in CYP2A6 or CYP2C9 DNA comprising:

- 10 (a) amplifying an exon containing a variant sequence with in said DNA, producing an extension product;
- (b) treating extension products with at least one restriction endonuclease under conditions sufficient to produce digestion fragments;
- 15 (c) analyzing the digestion fragments, for a variant specific digestion fragment or lack thereof.

9. The method of claim 8 wherein a CYP2C9 variant DNA is being detected.

20 10. The method of claim 9 wherein the amplifying step is a polymerase chain reaction using primers comprising HF18 and HF2R.

25 11. The method of claim 8 wherein step (a) is preceded by a gene-specific amplification reaction.

12. The method of claim 11 wherein the gene-specific amplification is a polymerase chain reaction.

30 13. The method of claim 12 wherein a CYP2A6 variant is being detected.

35 14. The method of claim 13 wherein a gene-specific amplification reaction uses primers comprising F4 and R4 and the exon amplification reaction uses primers comprising E3F and E3R.

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15. The method according to claim 10 wherein the extension products are treated with the restriction endonuclease *AvaII*.

16. The method according to claim 14 wherein the extension products are treated with at least one restriction endonuclease comprising *DdeI* and *XcmI*.

17. A method of determining the presence or absence of an allelic variant in CYP2A6 or CYP2C9 DNA comprising:

- (a) contacting said DNA with a first primer encompassing a nucleotide variation specific to variant DNA and a second primer which is complementary to a region of said DNA such that upon hybridization and amplification, an extension product will be formed;
- (b) analyzing the extension products for allelic-variant specific extension products.

18. The method of claim 17 wherein a CYP2A6 variant DNA is being detected.

19. The method of claim 18 wherein the amplifying step is a polymerase chain reaction wherein the first primer comprises J51 and J61 and the second primer comprises primer B.

20. A kit for determining the presence or absence of an allelic variant of CYP2A6 or CYP2C9 DNA comprising: at least one nucleic acid primer sequence capable of hybridizing to said DNA; the kit further containing instructions relating to the determination of the presence or absence of an allelic variant of CYP2A6 or CYP2C9 DNA.

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21. The kit according to claim 20 further comprising amplification components and at least one restriction endonuclease.

22. The kit of claim 20 wherein the CYP2A6 allelic variant is being detected.

23. The kit of claim 22 wherein the nucleic acid primers comprise F4, R4, E3F and E3R.

24. The kit according to claim 20 wherein the CYP2C9 allelic variant is being detected.

25. The kit according to claim 25 wherein the nucleic acid primers comprise HF18 and HF2R.

26. A process for providing a human with a therapeutic CYP2A6v2 or CYP2A13 DNA segment said human cells expressing in vivo in said human or therapeutically effective amount of said protein.

27. A pharmaceutical composition comprising an antisense nucleic acid derived from CYP2A6v2 DNA.

28. A pharmaceutical composition comprising and antisense nucleic acid derived from CYP2A13.

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.....exon 2.....	
IIc1 (C9)	GATCTTGGAGAGGAGTTTTCTGGAAAGAGGCAATTTCCACCTGGCT Asp Leu Gly Glu Phe Ser Gly Arg Gly Ile Phe Pro Leu Ala
IIc2 (C8)	GATAATGGAGAGGAGTTTTCTGGAAAGAGGCAATTTCCCAATACT Asp Asn Gly Glu Glu Phe Ser Gly Arg Gly Asn Ser Pro Ile Ser
DIIC2	
Clone 4 (hIIc1-4)	GATCTTGGAGAGGAGTTTTCTGGAAAGAGGCCAATTTCCACCTGGCTG
Clone 18 (hIIc1-18)	GATCATGGAGAGGAGTTTTCTGGAAAGAGGAAGTTTCCAGTGGCTG
Clone 3	
Clone 16	GATCATGGAGAGGAGTTTTCTGGAAAAGGTATTTCCCAGTATCCA
Clone 21 (hIIc1-21)	GATCTTGGAGAGGAGTTTTCTGGAAAGAGGCCAATTTCCACCTGGCTG
Clone 26 (hIIc1-26)	GATCATGGAGAGGAGTTTTCTGGAAAGAGGAAGTTTCCAGTGGCTG
Clone 33	

FIG. 1 (Sheet 1)

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IIIC1exon 2.....][Start of Intron 2.....
	GAAAGAGCTAACAGAGGATTG
IIIC2	Glu Arg Ala Asn Arg Gly Phe G
	CAAAGAATTACTAAAGGACTTG
	Gln Arg Ile Thr Lys Gly Leu G
DIIC2	CTTGGTAGGTGCACATATTCTGTGTCAGCTTTGGTAAC
Clone 4	AAAGAGCTAACAGAGGATTGGTAGGTG <u>IGCAAGTGGCTGTTTCAGCATCTGCTTGG</u>
	Primer HF-18
Clone 18	AAAAAAGTTAACAAAGGACTTGGTAATGTGCATGTATCGTGTGTATGTACATGT
Clone 16	AAAAAAGCTA GTAAGGAGTTGGTACATGTGTGTCAGTGTGTGCGCTTTGTCTG
Clone 21	AAAGAGCTAACAGAGGATTGGTAGGTGTGCAAGTGGCTGTTTCAGCATCTGCTTGG
Clone 26	AAAAAAGTTAACAAAGGACTTGGTAATGTGCATGTATCGTGTGTATGTACATGT

FIG. 1 (Sheet 2)

.....Intron 2.....

D11C2	TGGGGTGAGGGGGATGGAACACAGAGCCCTAAAAAGCTTCTCAGCAGAGCTTAGC	
Clone 4	GGATGGGAGGATGGAACACAGAGACTTACAGAGCTCCTCGGGCAGAGCTTGGCCA	
Clone 18	GTATGTACTGGGCAGTGGCTATAGGGATGGGAGGATGGAACACAGGCTTGAAAA	
Clone 3		CAGAAGGTGAAT(G)GAAACAACAC(T)TGAA
Clone 16	TATTAGTAATGAGGCAGAGGTGAATGGAACAAACACACTTGAAGAGCTCCTAAA	
Clone 21	GGATGGGAGGATGGAACACAGAT	CTA GCAGAGCT(T)]CTCGGG
Clone 26	GTATGTACTGGGCAGTGGCTATAGGGATGGGAGGATGGAACACAGGCTTGAAGA	

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FIG. 1 (Sheet 3)

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.....Intron 2.....

DIIC2 CTATCTGCATGGCTGCCAAGTGTGCAGCACATTCTTCCTTGGCTGTGAATTCTC

Clone 4 TCCACATGGCTGCCCAGTGTCAAGCTTCCTCTTTCTTGGCTGGGATCTCCCTCCTA

Clone 18 GCTCCTGGGACAGAACTTGACCTGTCCACGTGGCTGCCGAGTGTCAAGCTCTCTTG

Clone 3 GAGCTCCTAAAC(T)TAGC(T)TAGCTTGGCCATTGGGTGGCTGTTGAAAATCAGCTTC

Clone 16 ACTTAGCTTGGCC(C)ATTTGGTGGCTGTTGAAATCAGCTTCCTCTTCNNNC(C)TGG

Clone 21 CAGAGCTTGGCCCATCCACATGGCTGCCCAGTGTCAAGCTTCCTCTTTCTTGGCTG

]Clone 26 GCTCCTGGGACAGAACTTGACCTGTCCACGTGGCTGCCGAGTGTCAAGCTCTCTTG

FIG. 1 (Sheet 4)

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.....end of intron 2]

DIIC2	CCAGTTTCIGCCCCCTTTTATTATAG	
Clone 4	GTTTCGTTTCTCTTCCTGTTAG	
Clone 18	TCCTTGTTTGGATTCTCCCTCGTAGCTTCTGTTTTCTGTTCTGCTAG	
Clone 3	CTCTTTCTTGGCTGGGATCTCCCTCCTCGTTTCTGTTTCCCTTCCTTTCA	
Clone 16	ATCTCCTCCCTCGTTTCTGTTCCCTCCCTC	A
Clone 21	GGATCTCCCTCCTAGTTTTCGTTTCTCTTCCCTGTT	AG
Clone 26	TCCTTGTTTGGATTCTCCCTCGTAGCTTCTGTTTTCTGTTCTGCTAG	

FIG. 1 (Sheet 5)

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[Start of exon 3.....]

IIC1	GAATTGTTTTCAGCAATGGAAAGAAATGGAAGGAGATCCGGCGTTTCTCCCTCATGACG	
	ly Ile Val Phe Ser Asn Gly Lys Lys Trp Lys Glu Ile Arg Arg Phe Ser Leu Met Thr	
IIC2	GAATCATTTTCCAGCAATGGAAAGAGATGGAAAGGAGATCCGGCGTTTCTCCCTCACAACC	
	ly Ile Ile Ser Ser Asn Gly Lys Arg Trp Lys Glu Ile Arg Arg Phe Ser Leu Thr Thr	
DIIC2	GAATCATTTTCCAGCAATGGAAAGAGATGGAAAGGAGATCCGGCGTTTCTCCCTCACAACC	
Clone 4	GAATTGTTTTCAGCAATGGAAAGAAATGGAAGGAGATCAGGCGTTTCTCCCTCATGACG	
Clone 18	GAATCCTTTTTCAGCAATGGAAAGAGATGGAAAGGAGATCCGGCGTTTCTGCCCTCATGACT	
Clone 3	GGATCATTTTTCAGCAATGGAAAGAGATGTAAGGATGTTCTGGCTCTTCTTGCTCATGACG	
Clone 16	GGATCATTTT	
Clone 21	GAATCGTTTTCAGCAATGGAAAGAGATGGAAAGGAGATCCGGCGTTTCTCCCTCATGACG	
Clone 26	GAATCCTTTTTCAGCAATGGAAAGAGATGGAAAGGAGATCCGGCGTTTCTCCCCCATGACG	
Clone 33		G T T

FIG. 1 (Sheet 6)

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IIIC1exon 3.....	CTGCGGAAATTTTGGGATGGGGAAGAGGAGCATTTGAGGACCTGTGTTCAAGAGGAAGCCCCG
IIIC2		Leu Arg Asn Phe Gly Met Gly Lys Arg Ser Ile Glu Asp Cys Val Gln Glu Glu Ala Ar
		TTGCGGAAATTTTGGGATGGGGAAGAGGAGCATTTGAGGACCGTGTTC AAGAGGAAGCTCA
		Leu Arg Asn Phe Gly Met Gly Lys Arg Ser Ile Glu Asp Arg Val Gln Glu Glu Ala Hi
		↑
DIIC2	TTGC	Site of A ₁₄₄ C polymorphism
Clone 4		CTGCGGAAATTTTGGGATGGGGAAGAGGAGCATTTGAGGACCGTGTTC AAGAGGAAGCCCCG
Clone 18		CTGCGGAAATTTTGGGATGGGGAAGAGGAGCATTCGAGGACCGTGTTC AAGAGGAAGCCCCG
Clone 3		CTCTGGAAATTTGTAGGATGGTGAAGAGGAGCAATGGAGA TGTTCAAGGTGAAGCCCCA AGCA
Clone 21		CTGCGGAAATTTTGGGATGGGGAAGAGGAGCATTTGAGGACCGTGTTC AAGAGGAAGCCCCG
Clone 26		CTGCGGAAATTTTGGGATGGGGAAGAGGAGCATTTGAGGACCGTGTTC AAGAGGAAGCCCCG
Clone 33		C

FIG. 1 (Sheet 7)

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2A6 Intron 2	-----GT GGCAGAGAG GGGAAAGGTGG GCAGGTGGAC GGAATGCTC	42
2A8 Intron 2	GTGAGGGGGT GGCAGAGAG GGGAAAGGTGG GCAGGTGGAT GGAATGCTC	49
2A7 Intron 2	-----GT GGCAGAGAG GGGAAAGGTGG GCAGGTGGAC GGAATGCTC	41
Consensus	GTGAGGGGGT GGCAGAGAG GGGAAAGGTGG GCAGGTGGAT GGAATGCTC	50
2A6 Intron 2	CGGTGTTCC AGCTTTTCTCC CTGACTCTCC TGCCTACTGG AGGTTTTCGG	92
2A8 Intron 2	CGGTGTTCC AGCTTTTCTCC CTGACTCTCC TGCCTACTGG AGGTTTTCGG	99
2A7 Intron 2	CGGTGTTCC AGCTTTTCTCC CTGACTCTCC TGCCTACTGG AGGTTTTCGG	91
Consensus	CGGTGTTCC AGCTTTTCTCC CTGACTCTCC TGCCTACTGG AGGTTTTCGG	100
2A6 Intron 2	AGATCCCCGA GCTGGTCTT CTTCTCCCAT CTCCTCTCAT TGGGGTCTC	142
2A8 Intron 2	AGATCCCCGA GCTGGTCTT CTTCTCCCAT CTCCTCTCAT TGGGGTCTC	149
2A7 Intron 2	AGATCCCCGA GCTGGTCTT CTTCTCCCAT CTCCTCTCAT TGGGGTCTC	141
Consensus	AGATCCCCGA GCTGGTCTT CTTCTCCCAT CTCCTCTCAT TGGGGTCTC	150
2A6 Intron 2	CGTGTGTAT CCCCACCTG TCTCCAGCC CCGGTCTTG ATTCCTCTC	192
2A8 Intron 2	CGTGTGTAT CCCCACCTG TCTCCAGCC CCGGTCTTG ATTCCTCTC	199
2A7 Intron 2	CGTGTGTAT CCCCACCTG TCTCCAGCC CCGGTCTTG ATTCCTCTC	190
Consensus	CGTGTGTAT CCCCACCTG TCTCCAGCC CCGGTCTTG ATTCCTCTC	200
2A6 Intron 2	CGCTCTCTCT GGGCCAGTC GTATTCTCT CTCATGGAG TCTCTCTTA	242
2A8 Intron 2	CGCTCTCTCT GGGCCAGTC GTATTCTCT CTCATGGAG TCTCTCTTA	249
2A7 Intron 2	CGCTCTCTCT GGGCCAGTC GAGTTCTCT CTCATGGAG TCTCTCTTA	239
Consensus	CGCTCTCTCT GGGCCAGTC GTATTCTCT CTCATGGAG TCTCTCTTA	250
2A6 Intron 2	CGCTCTCTCT TCCATCTCA AGGACATCT GGGTTTCTCT TTACCAGCC	292
2A8 Intron 2	CGCTCTCTCT TCCATCTCA AGGACATCT GGGTTTCTCT TTACCAGCC	299
2A7 Intron 2	CGCTCTCTCT TCCATCTCA AGGACATCT GGGTTTCTCT TTACCAGCC	267
Consensus	CGCTCTCTCT TCCATCTCA AGGACATCT GGGTTTCTCT TTACCAGCC	300
2A6 Intron 2	TGGGTCTCTG TCTACATGAG TCTTTGATC GGTCTTAGCT TCTGGGCTC	342
2A8 Intron 2	TGGTCTCTG TCTTCACTTG TCTTTGATC GGTCTTAGCT TCTGTGCTC	349
2A7 Intron 2	-----TCTTTGATC GGTCTTAGCT TCTGTGCTC	271
Consensus	TGGKYCTCTG TCTWCAKMG TCTTTKGC SCTCTYAGCT TCTGKCTC	350
2A6 Intron 2	TCTGGGTTTC TCATCTCTCC GGATCCCTTC CTCATTTCTT CCTCTCTCTT	392
2A8 Intron 2	TCCGTGTTTC TCTCTCTCT GTTCCCTCTT CCCACTTCTT CCTCTCTCTT	399
2A7 Intron 2	-----TCTCTCTCT GTTCCCTCTT CCTCTCTCTT	271
Consensus	TCYGGGTTTC TCTCTCTCT GSWCCCTTC CYCATTTCTT CCTCTCTCTT	400
2A6 Intron 2	AGGATGCCAG GGTATTCTT ACTTCCACAT CTCAGGCTC CATCTCTCTG	442
2A8 Intron 2	AGGATTTTCAG GGT-ATTCTT ACTTCCACAT CTCAGGCTC CAATCTCTG	448
2A7 Intron 2	-----GTTATTCTT ACTTCCACAT CTCAGGCTC CAATCTCTG	271
Consensus	AGGATKYCAG GGTATTCTT ACTTCCACAT CTCAGGCTC CAATCTCTG	450
2A6 Intron 2	TAACAGTCTC TCTTCTCTCC AGACCTCTCT TTTTCTATC TCAATATTAA	492
2A8 Intron 2	TAATCTCTCT TCTTCTCTCC CGATCTCTCT TTTTCTCTC TCAATATTAA	498
2A7 Intron 2	-----TCTTCTCTCC TTTTCTCTC TCAATATTAA	271
Consensus	TAAKNGTCTC TCTTCTCTCC HGAYCTCTCT TTTTCTATC TCAATATTAA	500
2A6 Intron 2	ACTCTCT--G CTCAGGCTCA GGTTAAGAA CTACACCAA GAGAGGATCT	540
2A8 Intron 2	TCTCTCTCTT CTCAGGCTCA GGTTAAGAA CTACACCAA TTTTATTCT	546
2A7 Intron 2	-----CTCAGGCTCA GGTTAAGAA CTACACCAA	271
Consensus	WCTCTCTCTK CTCAGGCTCA GGTTAAGAA CTACACCAA GAKKKATCT	550

FIG. 2 (Sheet 1)

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2A6 intron 2	CCTCCACCCA	GATCTCCCCA	TATCTCACTA	CCCCACCCTC	CATC---CTC	587
2A8 intron 2	CCTCCTCCCC	GATCTCCCCA	TATCTCACTT	CCCCTCCTTC	CATCTCTCTC	596
2A7 intron 2	-----	-----	-----	-----	-----	271
Consensus	CCTCCWCCA	GATCTCCCCA	TATCTCACTW	CCCCWCCCTC	CATCTCTCTC	600
2A6 intron 2	TGCCT----C	CATCAC--TC	TCTTTCTC--	-----TCC	CC--A-----	613
2A8 intron 2	TTTCTCTCCC	CACTACCTTC	CCTTCCTCCA	TGGAGTATCC	CCGTATCCCT	646
2A7 intron 2	-----	-----	-----	-----	-----	271
Consensus	TKYCTCTCCC	CAYYACCTTC	YCTTYCTCCA	TGGAGTATCC	CCGTATCCCT	650
2A6 intron 2	CTGCCCCCTGC	GGACGCGATC	CAATGG--AG	TGTG-----	----GA---G	650
2A8 intron 2	CTGTTTCTCT	GCACTCTGTCT	GTCTGCCCTT	TCTGCTTCTC	TTCTGATTCT	696
2A7 intron 2	-----	-----	-----	-----	-----	271
Consensus	CTGYYYCTSY	GSAYSYGWYY	SWMTGGCCWK	TSTGCTTCTC	TTCTGATTCK	700
2A6 intron 2	CTAATGCCGT	-----GAA	GCTATGTGCA	TCTCTCTGTC	TGGCCGTACC	693
2A8 intron 2	CTTATTCTTT	CTACCCGGAC	TCTCTCTCTC	TCTCTCTCTC	TCTCTCTCTC	746
2A7 intron 2	-----	-----	-----	-----	-----	271
Consensus	CTWATKCYKT	CTACCCGGAM	KCTMTSTSYM	TCTCTCTSTC	TSKCYSTMVC	750
2A6 intron 2	TGGGT---AA	TAACCTGATC	GACT-----	-----	-----	714
2A8 intron 2	TCTCTCTCTC	TCTCTCTCTC	TCTCTCTCTC	TCTCTCTCTA	TATATATATA	796
2A7 intron 2	-----	-----	-----	-----	-----	271
Consensus	TSKSTCTCWM	TMWCYYKMT	KMYTCTCTC	TCTCTCTCTA	TATATATATA	800
2A6 intron 2	-----	-----	-----	-----	-----	714
2A8 intron 2	TATATATATA	CACACACACA	CACACACACA	CACACACACA	CACACACATA	846
2A7 intron 2	-----	-----	-----	-----	-----	271
Consensus	TATATATATA	CACACACACA	CACACACACA	CACACACACA	CACACACATA	850
2A6 intron 2	-----	-----	-----	-----	-----	714
2A8 intron 2	TATATTAGGG	GGGGACTCCC	TTTCTGCTCC	ACCCTTGGGG	AGCCCCCTGG	896
2A7 intron 2	-----	-----	-----	-----	-----	271
Consensus	TATATTAGGG	GGGGACTCCC	TTTCTGCTCC	ACCCTTGGGG	AGCCCCCTGG	900
2A6 intron 2	-----	-----	-----	-----	-----	714
2A8 intron 2	AACTGGTCCG	CTCTGCTACC	ACCACCCCT	GACCTCTCTC	CACCCCTGCG	946
2A7 intron 2	-----	-----	-----	-----	-----	271
Consensus	AACTGGTCCG	CTCTGCTACC	ACCACCCCT	GACCTCTCTC	CACCCCTGCG	950
2A6 intron 2	-----	---	---	---	---	714
2A8 intron 2	TTCACCTCCC	CA	---	---	---	958
2A7 intron 2	-----	---	---	---	---	271
Consensus	TTCACCTCCC	CA	---	---	---	962

Intron 2 alignment

FIG. 2 (Sheet 2)

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2A8 exon 3	GCSTGGCCTT	CAGGAACGGG	GAGCGCGGCA	AGCAGGTCCT	GGGCTTTCCT	50
2A6 exon 3	GCSTGGTATT	CAGGAACGGG	GAGCGCGGCA	AGCAGGTCCT	GGGCTTTCCT	50
2A7 exon 3	GCSTGGCCTT	CAGGAACGGG	GAGCGCGGCA	AGCAGGTCCT	GGGCTTTCCT	50
Consensus	GCSTGGCTT	CAGGAACGGG	GAGCGCGGCA	AGCAGGTCCT	GGGCTTTCCT	50
2A8 exon 3	ATCGCCACCC	TTAGGGGACTT	GGGCTGGGC	AAGCGGGCA	TCGAGGAGCG	100
2A6 exon 3	ATCGCCACCC	TTAGGGGACTT	GGGCTGGGC	AAGCGGGCA	TCGAGGAGCG	100
2A7 exon 3	ATCGCCACCC	TTAGGGGACTT	GGGCTGGGC	AAGCGGGCA	TCGAGGAGCG	100
Consensus	ATCGCCACCC	TTAGGGGACTT	GGGCTGGGC	AAGCGGGCA	TCGAGGAGCG	100
Codon 160						
2A8 exon 3	CATCCAGGAG	GAGCGGGCT	TCTCATCGA	GGCCTCCGG	AGCAGGCACG	150
2A6 exon 3	CATCCAGGAG	GAGCGGGCT	TCTCATCGA	GGCCTCCGG	AGCAGGCACG	150
2A7 exon 3	CATCCAGGAG	GAGCGGGCT	TCTCATCGA	GGCCTCCGG	AGCAGGCACG	150
Consensus	CATCCAGGAG	GAGCGGGCT	TCTCATCGA	GGCCTCCGG	AGCAGGCACG	150
← Primer J51/61 →						

Exon 3 alignment

FIG. 2 (Sheet 3)

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2A8 intron 3	-----	-----	-----	G	AGAGTAGGGG	ACCTGAGTG	21	
2A6 intron 3	GTGAGCAGGG	GACCCCGAGT	GCGGGGGCGG	G	GAGTAGGGA	ACCTGAGTG	44	
2A7 intron 3	GTGAGTAAGG	TTCCCGAGT	GCGGGGGCGG	G	GAGTAGGGA	ACCTGAGTG	44	
Consensus	GTGAGYARGG	KWCCCGAGT	GCGGGGGCGG	G	TGAGTAGGGA	ACCTGAGTG	50	
2A8 intron 3	CGAGGTCG	G	GAACCGCG	G	GCTTCTGCG	TGGGATGGG	GACTAGGTGG	68
2A6 intron 3	CGAGGTCG	G	GAACCGCG	G	GCTTCTGCG	TGGGATGGG	GACTAGGTGG	94
2A7 intron 3	CGAGGTCG	G	GAACCGCG	G	GCTTCTGCG	TGGGATGGG	GACTAGGTGG	94
Consensus	CGAGGTCG	G	GAACCGCG	G	GCTTCTGCG	TGGGATGGG	GACTAGGTGG	100
2A8 intron 3	GGAAAGGGGC	CCGCACTTCC	AGCCCTGGAG	TCTGGCGCT	GGATTTGGG	117		
2A6 intron 3	GGAAAGGGGC	CCGCACTTCC	AGCCCTGGAG	TCTGGCGCT	GGATTTGGG	144		
2A7 intron 3	GGAAAGGGGC	CCGCACTTCC	AGCCCTGGAG	TCTGGCGCT	GGATTTGGG	144		
Consensus	GGAAAGGGGC	CCGCACTTCC	AGCCCTGGAG	TCTGGCGCT	GGATTTGGG	150		
2A8 intron 3	TCAACAGGGC	CCTGCCCTCCT	GGAATTCTGA	CTCTCCTCAG	ACCTCTGAGT	167		
2A6 intron 3	TCAACAGGGC	CCTGCCCTCCT	GGAATTCTGA	CTCTCCTCAG	ACCTCTGAGT	194		
2A7 intron 3	TCAACAGGGC	CCTGCCCTCCT	GGAATTCTGA	CTCTCCTCAG	ACCTCTGAGT	194		
Consensus	TCAACAGGGC	CCTGCCCTCCT	GGAATTCTGA	CTCTCCTCAG	ACCTCTGAGT	200		
← Primer B →								
2A8 intron 3	TGACTCTCTC	CCCAACCCCC	CTTCTCCCGC	CATACCTGTA	207			
2A6 intron 3	TGACTCTCTC	CCCAACCCCC	T-TCTCCCGA	CATACCTGTA	233			
2A7 intron 3	TGACTCTCTC	CCCAACCCCC	TCCTCCCTC	CATACCTGTA	235			
Consensus	TGACTCTCTC	CCCAACCCCC	YYCTCCCKM	CATACCTGTA	241			

Intron 3 alignment

FIG. 2 (Sheet 4)

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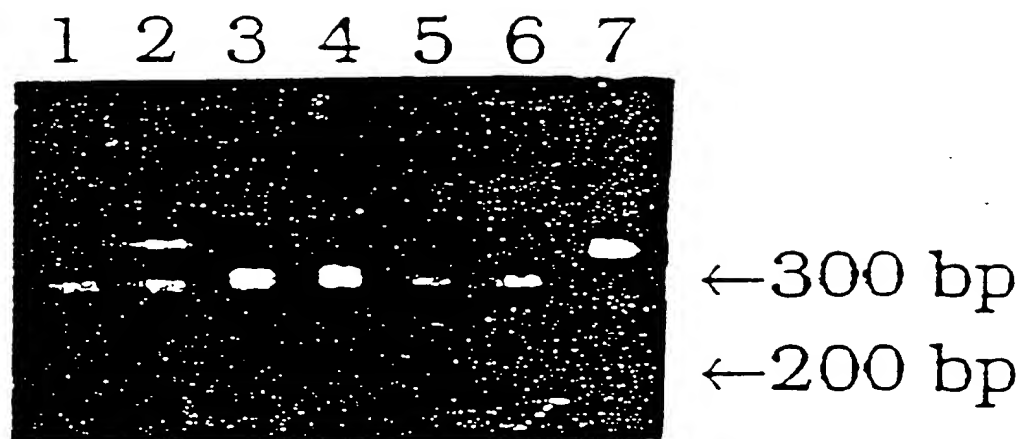
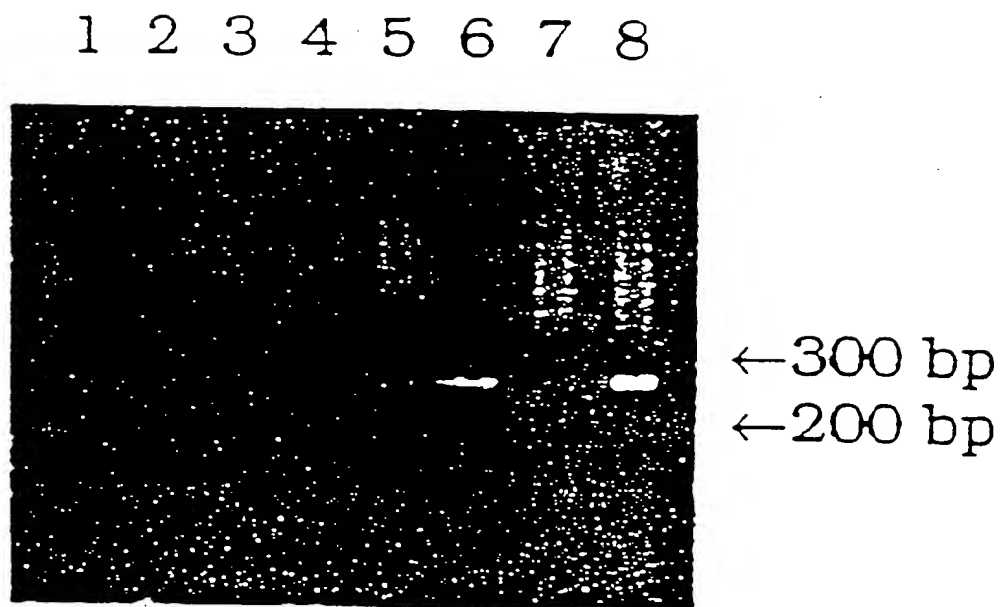


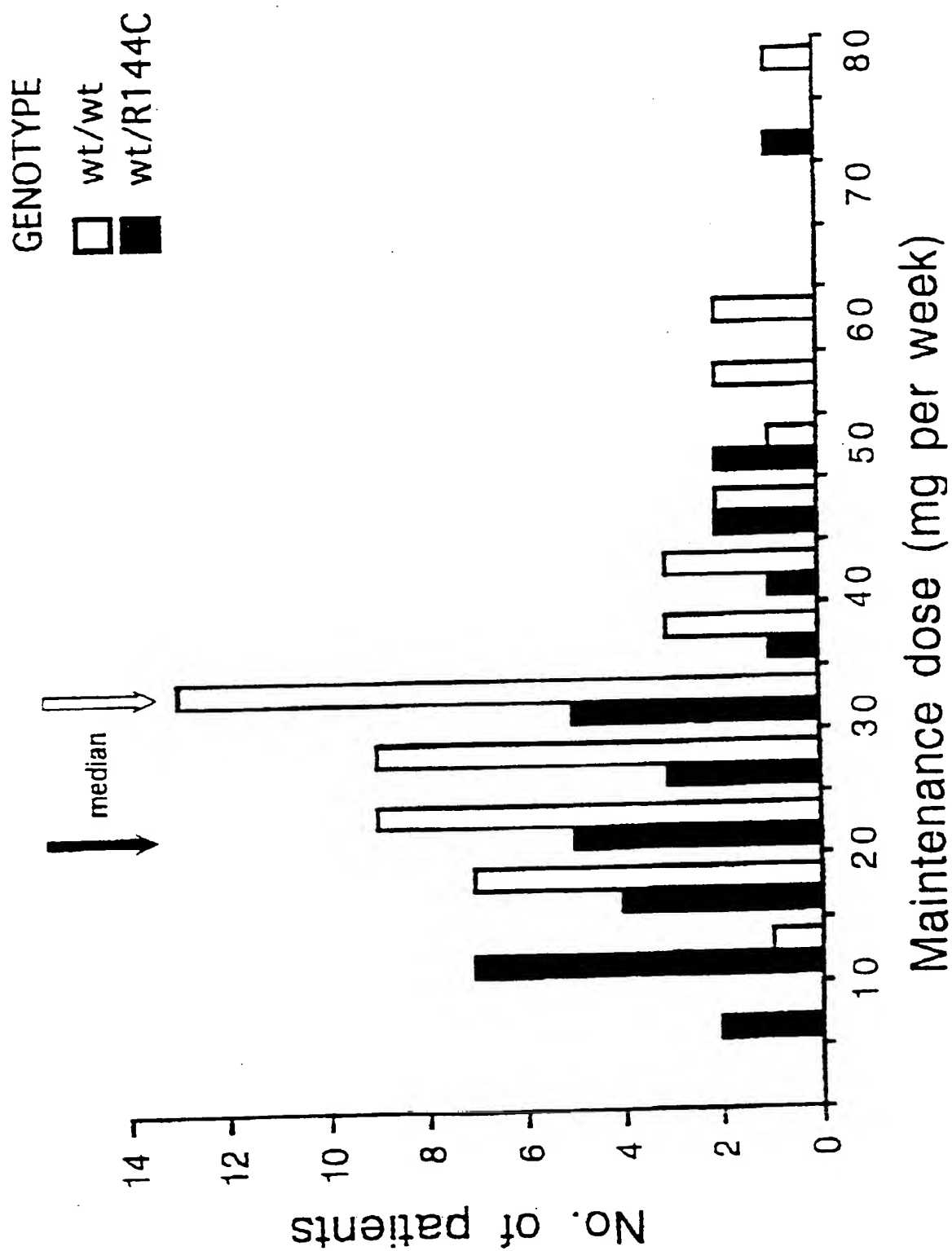
FIG. 3

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**FIG. 4**

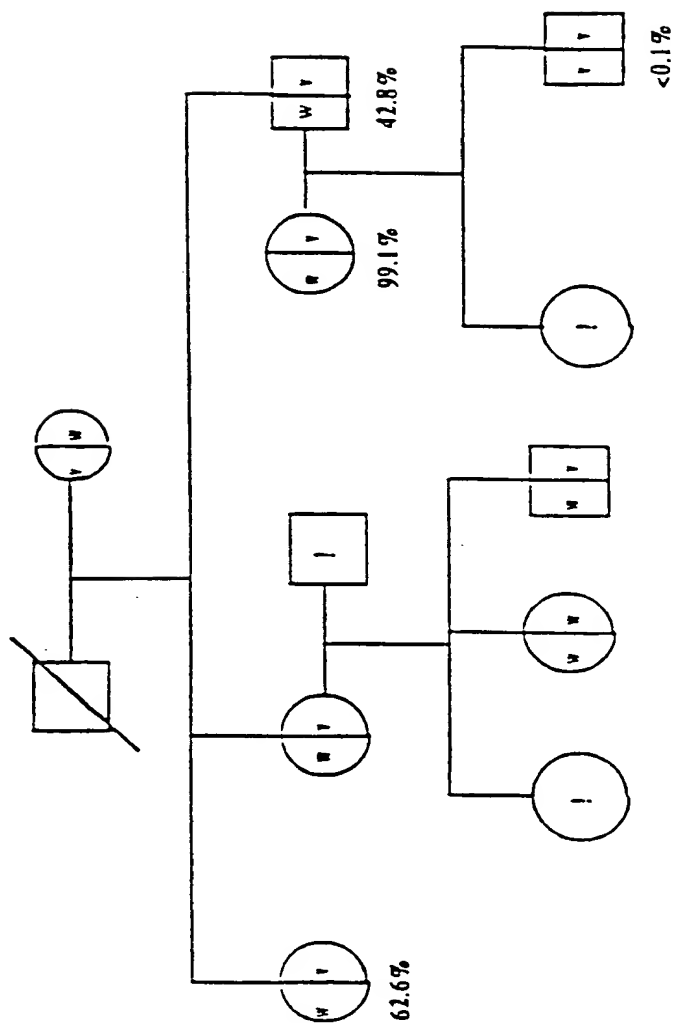
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FIG. 5



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7-Hydroxylation of coumarin (%) in a family genotyped for the presence of *CYP2A6* and *CYP2A6v* alleles, showing subject homozygous for *CYP2A6v* who is deficient in coumarin 7-hydroxylation

w = *CYP2A6* wild-typev = *CYP2A6v* mutant allele

γ = not determined

FIG. 6

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2A6 cDNA	GCGTGGTATT	CAGCAACGGGGAGCGGCCCAAGCAGCTCCGGCGCTTCTCCAT		
2A6 gene			T	TG
2A6 cDNA	CGCCACCCTGCGGGACTT	CGGGTGGGCAAGCGAGGCATCGAGGAGCGGCATC		
2A6 gene			A	C
2A6 cDNA	CAGGAGGAGCGGGCTT	CCCTCATCGACGCCCTCCGGGGCACTGGC		
2A6 gene			T	G A A GCA

Comparison of CYP2A6 cDNA and genomic sequences for exon 3

FIG. 7

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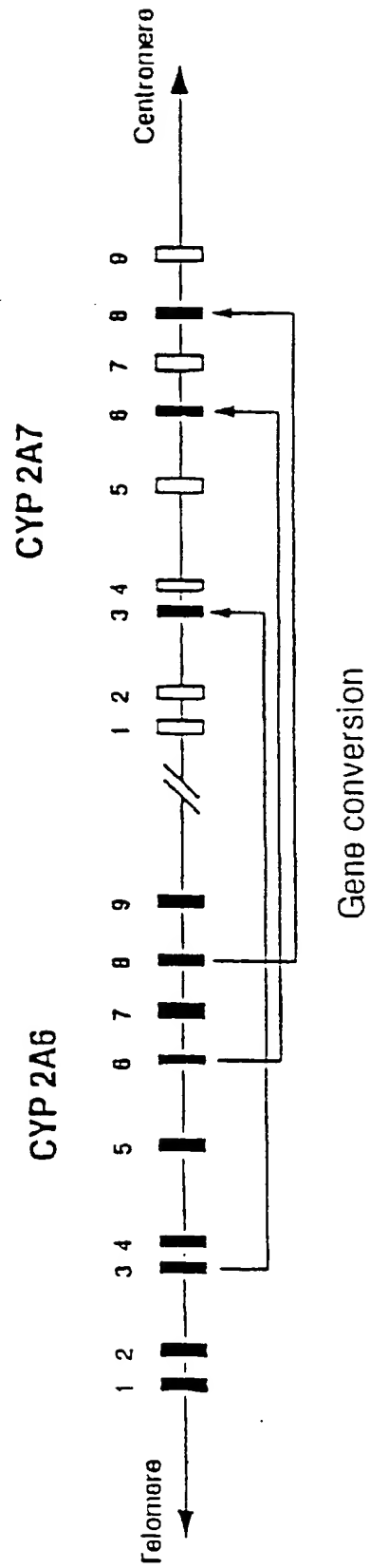


FIG. 8A

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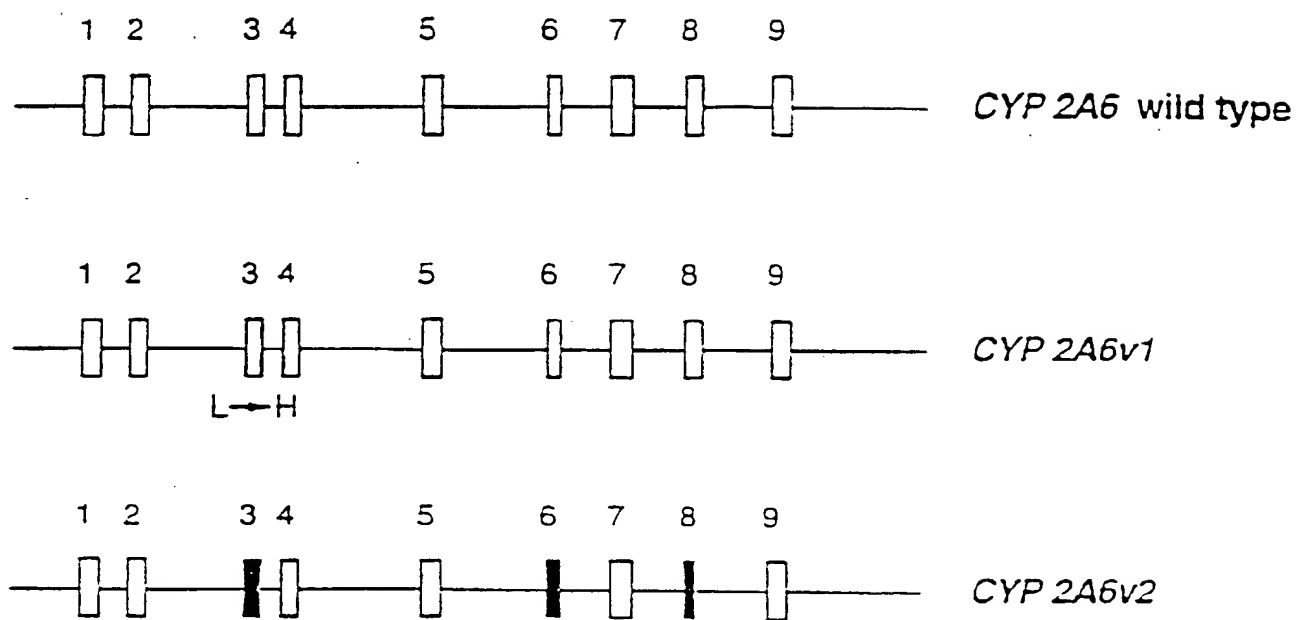


FIG. 8B

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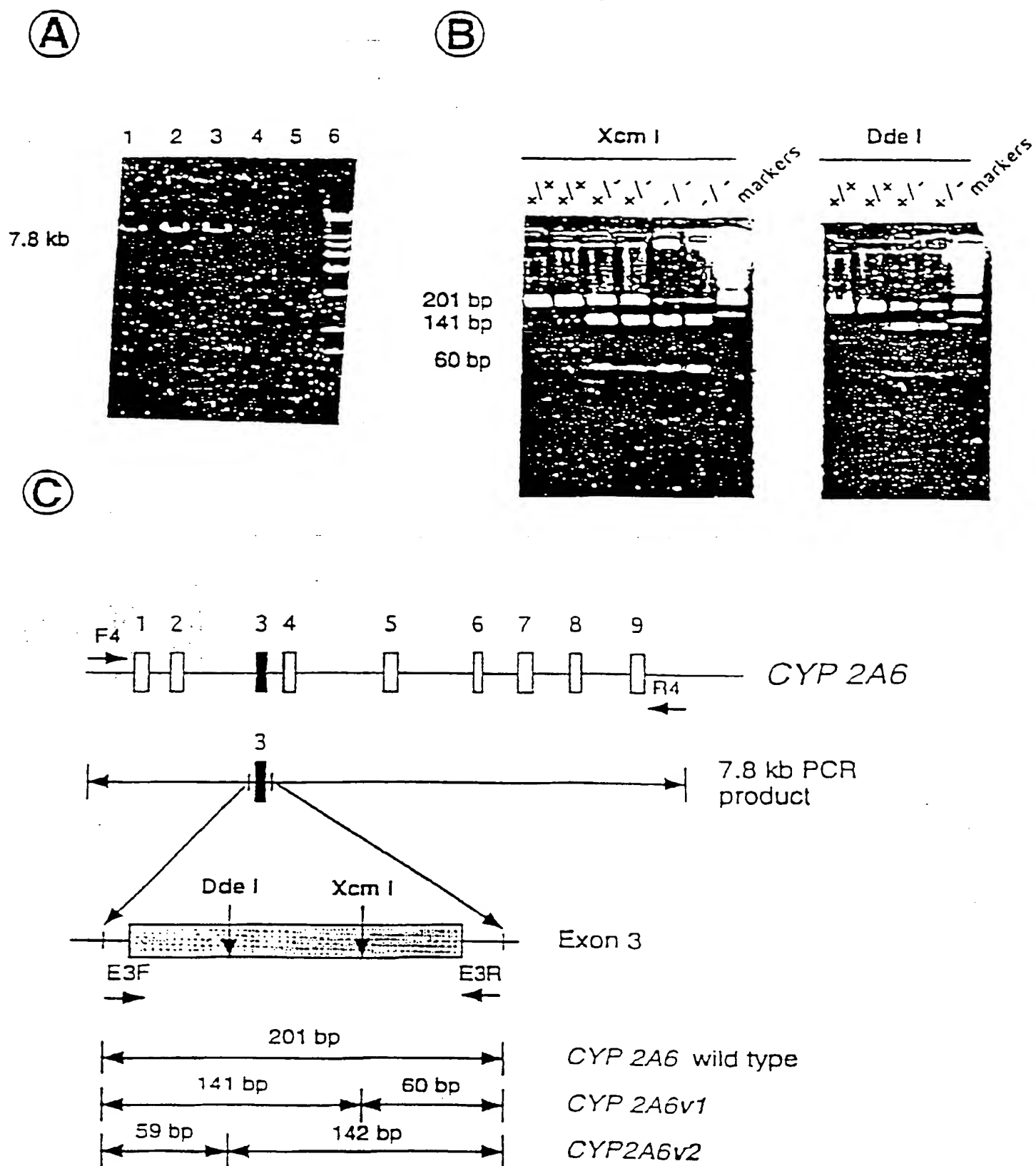


FIG. 9

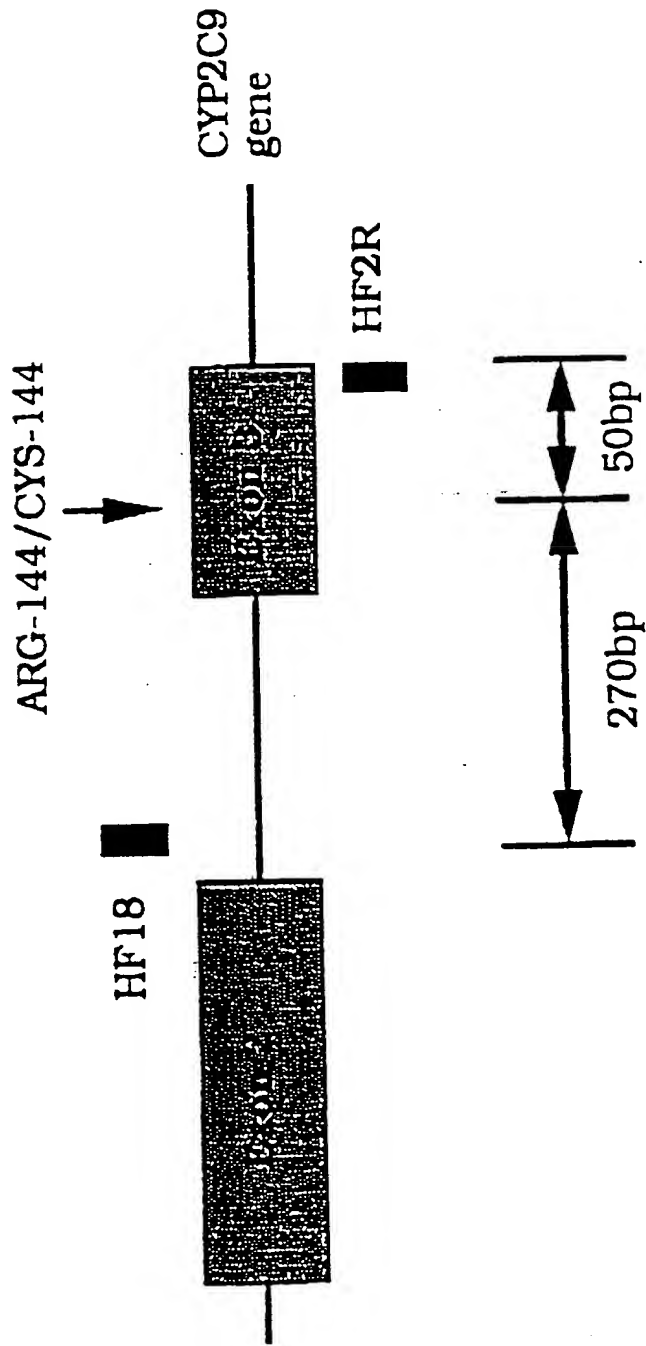


FIG. 10

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CYP2A6v2 cDNA.

5'TCTACCACCATGCTGGCCTCAGGGATGCTTCTGGTGGCCTTGCTGGCCTGCT
GACTGTGATGGTCTTGATGTCTGTTTGGCAGCAGAGGAAGAGCAAGGGGAA
GCTGCTOOCGGGACCCACCCCATTTGCOCTTCATTGGAACTACCTGCAGCTGA
ACACAGAGCAGATGTACAACCTOCTCATGAAGATCAGTGAGCGCTATGGCC
COGTGTTCACCATTCACTTGGGGGCCCCGGGGTGGTGGTGGTGTGTGGACATG
ATGCOGTCAAGGAGGGCTCTGGTGGACCAAGGCTGAGGAGTTCAGCGGGGAGGCG
GAGCAAGCCACCTTOGACTGGGTCTTCAAAGGCTATGGCGTGGTATTACAGCA
ACGGGGAGCGGCGCAAGCAGCTOCTGCGCTTTGOCATCGCCACCTGAGGGACT
TOGGGGTGGGCAAGCGAGGCATCGAGGAGCGCATOCAGGAGGAGTGGGGCTTC
CTCATOGAGGGCCATCCGGAGCAACGCAACGGCGCCAATATOGATCCACCTTCTTC
CTGAGCCGCACAGTCTCCAATGTTCATCAGCTCCATTGTCTTTGGGGACCGCTT
TGACTATAAGGACAAAGAGTTCTCTGTCACTGTTGCGCATGATGCTAGGAAT
CTTCCAGTTCACGTCAACCTCCACGGGGCAGCTCTATGAGATGTTCTCTTOGG
TGATGAAACACCTGOCAGGACCACAGCAACAGGCCTTTCAGTTGCTGCAAGG
GCTGGAGGACTTCATAGCCAAGAAGGTGGAGCACAACCAGCGCACGCTGGA
TOCCAATTCCCCACGGGACTTCATTGACTOCTTTCTCATCCGCATGCAGGAGG
AGGAGAAGAACCCCAACACGGAGTTCTACTTGAAGAACCTGATGATGAGC
ACGTTGAACCTCTTCATTGCAGGCCACCGAGACGGTCAGCACCAOCTGCACTA
TGGCTTCTTGCTGCTCATGAAGCACCCAGAGGTGGAGGCCAAGGTCCATGAG
GAGATTGACAGAGTGATCGGCAAGAACCGGCAGCCCAAGTTTGAGGACCGG
GCCAAGATGCCCTACATGGAGGCAGTGATCCACGAGATCCAAAGATTTGGA
GACGTGATCCCATGAGTTTGGCCCGCAGAGTCAAAAAGGACACCAAGTTTC
GGGATTTCTTCTOCTOCTAAGGGCATAGAAGTGTTCCCTATGTTGGGGCTCCGTG
CTGAGAGACCTCAGGTTCTTCTOCCAACCCCCGGGACTTCAATOCCAGCACTTC
CTGGGTGAGAAGGGGCGAGTTTAAGAAGCGTGATGCTTTTGTGCCCTTCTCCA
TCAGAAAGCGGAAGTGTTCGGGAGAAGGCCTGGCCAGAATGGAGCTCTTTCT
CTTCTTCACCAACCGTCATGCAGAACTTCGCTCAAGTCTOCCAGTCACTA
AGGACATTGACGTGTCCCCCAACACGTGGGCTTTGCCACGATCCCAAGAAA
CTACAOCATGAGCTTCTGCCCCGCTGAGCGAGGGCTGTGCGGTGAAGGTCTG
GTGGGCGGGGCCAGGGAAGGGCAGGGCCAAGACCGGGCTTGGGAGAGGGGC
GCAGCTAAGACTGGGGGCAGGATGGCGGAAAGGAAGGGGCGTGGTGGCTAG
AGGGAAGAGAAGAAACAGAAGCGGCTCAGTTACCTTGATAAGGTGCTTCC
GAGCTGGGATGAGAGGAAGGAAACCCTTACATTATGCTATGAAGAGTAGT
AATAATAGCAGCTCTTATTTCTGA 3'

FIG. 11

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1  AAGTTCCCCT GAAATATGGC TCTGGTCTTC CTCCCCTTGC CAATGAAGAA GATGGCAGTG
61  GAGGTTCTAT GGCAGCCATC CTGGCCTCAC TCTGAGGTTT CAATGAGGAT TCTGGGCATC
121 AAGAGACAGC TCTGGGCAAA GCTAAATCAA GTGAGCCCTT GGACCCAGTG CTGGGCTGCT
181 GGGCTTTCTG GGAGAACGCC GCTGGGCTTG CTACACACTC CTCCTCCAG AAACTCCACA
241 CCCACAGCCC TGGGTCTTCC TAGCCCGAG ACTTTCAAGT CCATATGCCT GGAATCCCCC
301 TTCCTGAGAC CCTTAACCCCT GCATCCTCCA CAACAGAAGA CCCCTAAATG CACAGCCACA
361 CTTTGTCTTA CCCTAATAAA ACCCAGACCT TTGGATTCTT CTCCCCTGGA ACCCCCAGAT
421 CCGCACAACT TTGGGGTGCA TTCTCACTCT CAGACCCCAA ATCCAAAGCC CAAGTGCTCC
481 CCTATGCAAA TATTCCAAAC TCCTCAGTTC TACAGCTTAT CTGTGCCCCC CTCCTAAATC
541 CACAGCCCTG CGCCACCCCT CCTGAAGTAC CACAGATTTA GTCTGGAGGC CCCCTCTCTG
501 TTCAGCTGCC CTGGGGTCCC CTTATCCTCC CTTGCTGGCT GTGTCCCAAG CTAGCCAGGA
661 TTCATGGTGG GGCATGTAGT TGGGAGGTGA AATGAGGTAA TTATGTAATC AGCCAAAGTC
721 CATCCCCTCT TTTCAAGCAG TATAAAGGCC AACCACCCCA GCCGTACCA TCTATCATCC
781 CTCTACCACC ATGCTGGCCT CAGGGATGCT TCTGGTGGCC TTGCTGGCCT GCCTGACTGT
841 GATGGTCTTC ATGTCTGTTT GGCAGCAGAG GAAGAGCAAG GGAAGCTGC CTCGGGACC
901 CACCCCATTG CCCTTCATTG GAAACTACCT GCAGCTGAAC ACAGAGCAGA TGTACAACTC
961 CCTCATGAAG GTGTCCCAAG ACAGGAGAT GSGTGTCTCG GGGTGGGGGC TGCCTAGTTG
1021 GCTGGGGCTT TGTGGCAGGG GGTTGACCAG TGTGGACCAG AGTCTTAGGA AATGGAGTTT
1081 TGGAGTTTCA GCATCAGAAA GACAGGATCT TGGGATGTCC AGCTCCCTGA CTGTGAGAAC
1141 CTGGGTGCGA AGCATCCCAG CACATGACAT CTCGGTGCTG GGCCCCATTC AGAGTGGAGG
1201 GTTCTCCCTC TAACCACTCC CACCCACCTC CATCAGATCA GTGAGCGCTA TGCCCCCGTG
1261 TTCACCATTC ACTTGGGGCC CCGGCGGGTC GTGGTCTGTG GTGGACATGA TGCCGTCAGG
1321 GAGGCTCTGG TGGACCAGGC TGAGGAGTTC AGCGGGCGAG GCGAGCAAGC CACCTTCGAC
1381 TGGGTCTTCA AAGGCTATGG TGCCCAAGAG GGGGAAGGTG GGCAGGTGGA CACGAAGGTC
1441 TCAGTGTTC CAGCCTCTTC CCTGACTCTC CTGACAAC TGAGGATAAGG GAGAGTCCCC
1501 AGTCTGGTCT TCCCTCCCCA TCTCCCTACA TTGGGGCCTC TCCATGTGTA TCCCTCACCT
1561 GTCTCCAGCG GCCCTGTCTT GATTCCTCCC TGCCCTCTCT TCCCCACCT CTTATTCTC
1621 TCTCACTGGA GTCTCCTCTT TCCCTCTCT CTCCATCTCT AAGGACATCC TGGGTTCTG
1681 TTTACCAGCC CTGGGTCTCT GTCTACATGA GTCTTTGAGG CCCTCTTACC TTCTGGGCTT
1741 CTCTGGGTTT CTCACTCTTC CGGATCCCTT TCTCAATTCT TCCTCTGTCT TAGGATGCCA
1801 GGGTTATTCC TACTTCCACA TCTTCAGGCT CCATCTCCTG GTAACAGTCT CTCTTCTTC
1861 CAGACCCCTC CTGTTTCTAT CTCAATATTA AACTCTCTGC TCCAGCTCAG CTTAAGAATC
1921 TCACACCAAG AGAGGATGTC CTCCACCCAG ATCTCCCCAT ATCTCACTAC CCCACCTCC
1981 ATCCTCTGCC TCCATCACTC TCTTCTCTC CCCACTGCNC CTGCGGACGC GATCCAAATG
2041 AGTGTGGAGC TAATGCCGTG AAGCTATGTG CATCTCTCTG TCTGGCCGTA CTTGGGTAAT
2101 AACCTGATCG ACTAGGCGTG GTATTCAAGCA ACGGGGAGCG CGCCAAGCAG CTCCTGCCCT
2161 TTGCCATCGC CACCCCTGAGG GACTTCGGGG TCGGCAAGCG AGGCATCGAG GAGCGCATCC
2221 AGGAGGAGTC GGCCTTCTCT ATCGAGGCCA TCCGGAGCAC GCACGGTGAG CAGGGGACCC
2281 CGAGTGCCGG GGCAGGAGAA GGAAAACACC CAGGACGAGG AACCCGCGCG CGTTCTGCCT
2341 GGGGATGGGG ACTAGGTGGG GAAAGGCCCC CGCACTTCCA GCCCTGGAGT CTGGCGCTGG
2401 GAATTGGGCT CAACAAGGCC CTGCTCTCTG GAATTCTGAC TCTCTCAGA CCTCTGAGTT
2461 GACTCTCTCC CCAACCCCTT TCTCCCGACA TACCCGGAGG CGCCAATATC GATCCACCTT
2521 TCTTCTGAG CCGCACAGTC TCCAATGTCA TCAGCTCCAT TGTCTTTGGG GACCGCTTTG
2581 ACTATAAGGA CAAAGAGTTC CTGTCACTGT TGCGCATGAT GCTAGGAATC TTCCAGTTCA
2641 CGTCAACCTC CACGGGGCAG GTAATGCTTG CAGCCCGGCC CGTGAAGGCC CTTACCAAAA
2701 CCGGCAAATT GTTCCCTTAC CGGGGAAGG GGGCCCCAAA TTCCACCGCG CCCCCGACA
2761 GTGTCCCCTC AAAATCAGTC CCGGATTTCG GCAAATTGGC AGAGTGAAC CAGACCCGGG
2821 TTGGTTGTCT AATCCCCTGC TCTCCAGGGA CACCGGGATA GCACAACAGA TGCTCCCCAA
2881 AACAGAGCCT GCTGGCAGGA TGCATACCCT CAGCTCAGCT CTCTACCCCT GGGCAGTGT
2941 TCCCATCCCC AACTTACCCG TAATTTCTAA CAGATGCTCC CTACCCAGGT CTTCTTGAAT
3001 ATTTTAACAC CCGGAAACCC TGGGTACCTA ACCTTCCCTG TAAACTTTAG AGATTAGTTC
3061 CTATCCGGCC CTTCTGAAAT ACCTAACCAC CGGAGACCAG ATGCCMTTAA CTCAGTTCTT
3121 TCCTTGCTAT GAAACAAATC CCATTCCCAT CAGCTCCTGC CCCGTGACAG CTGTCTTCTC
3181 CTTCCCATCC TCTCTCTGCA ACCCCAGCTC TATGAGATCT TCTCTTCGGT GATGAAACAC
3241 CTGCCAGGAC CGCAGCAACA GGCCTTTTCAG TTGCTGCAAG GGCTGGAGGA CTTTCATAGC
3301 AAGAAGGTGG AGCACAACCA GCGCACGCTG GATCCCAATT CCCCACGGGA CTTTCATTGAC
3361 TCCTTTCTCA TCCGCATGCA GGAGGTACAC CCCAGCAGCC ACTCGGGGGA GATGCAAGG

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FIG. 12 (Sheet 1)

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3421 CAGGCAGAGG GAAATCAGTC TGGGAGTGGG GCAGGCAGAT GACACAGGCC CATTCAAATT
3481 AACCCCTCATC ATAATAATCC TCACAATTGG CTGGGTGCCG TGGCTAACAG CCTGTAATCC
3541 CAGCACTTTG GGAGGCCGAG GCAGGTGGAT CACCTGAGGT CAGGAGTTCC AGACCAGCCT
3601 GGCCAACATG GTCAAACCCC GTCTCTACTA AAAATCCAAA AATTAGTTGG GCATGGTGGC
3661 GCGAAGGGGG GCAGAGGTTG CAATGAGCCA AGATCACGGC ATTGCACTCC AGTCTGGGTG
3721 ACAGAATGAG GCCCTGTGTC AAAAAAATT AATCACTTGT TTAAAAAGTA AGTGAGCCTG
3781 CATGGTTCATG CGCATGTGCA GCTCCAGCTA CTCAGGAGGC TGAGGCTGGA GGATTGCTTG
3841 AGCTCAGGAG TTGGCGTCCG GCCTGTGCAA CTTAGCAAGA CCAAGTCAGT ATAAGAAAAA
3901 AAAAAAACAA AAAAAAGCT GACAGCTAAG TTGATAATTG ACGGACAGAT CGTCAGCAAG
3961 GTAACGAAGG TGAGAAGGAA GAGCATTGGG GGCAACGCCA GGAGTCAGGG CAAGGGCTGG
4021 TTCCTACACC GAGTCTGGTA GGATCTAGGG CCCCTCTTCT CCACCCCTCG GTCTTGCCCC
4081 AAAGAGAGGT CGAGGGTGTCT GGGATTGGCG TAGACTCGAG TCTGTGTAGA TCTTGGGGTC
4141 CCCTCTTGAC CCCCATTTGGT CTGAACCTAA GAGTGGAAGA TCCATGGGGT GAACCCCTAG
4201 ATGGTGCCCT GAGGTCAAGC AGGAGTGAGG TTGTCTTAA GCCCCCTCTC GCTTCAGGAG
4261 GAGAAGAACC CCAACACGGA GTTCTACTTG AAGAACCCTGA TGATGAGCAC GTTGAACCTC
4321 TTCATTGCAG GCACCCGAGAC GGTCAACACC ACCCTGCACT ATGGCTTCTT ACTGCTCATG
4381 AAGCACCCAG AGGTGGAGGG TAAGCCTGGA GGGGGACGGA AGTGGAGGGC CCCAGACCCT
4441 CAAAATTTCC CTTCGACTGG TGCAATGTCC CCACCTGTCC CAGATCCCGG GACCCTGAGA
4501 CGTGACTTGC TGTCCAGAGA CAGGGCAACA TTCAGCTGGT AGGCATCAGC TGAGTCTCAT
4561 TAGATATTAA AATATTGAAA ATGTCTGCAC TGATTGGTCA GTCACTTCTG TCCCAAGCCC
4621 ACTGAGTGCC CACTGCCCGT TCCACCGGGT CATCCCCTAA GTTCCTCCCT GTGCTTCCCC
4681 TGTGATTCTG GCACAACCTG GTTAACAGGA TCCTACTCCA ACAATGCGAA TCGGTGATGT
4741 CTGTTCTGTT ATGAATGCTC TACTTCCGTC TCATAGGCCG AGGCATTTCA TCCACCCCAT
4801 TTTGCCTATC CGGACTATCA TTTCTGCTC TGAGACCCCT AGATACCTAA ACACATTCCC
4861 CCTCTCCCC CAGCCAAGGT CCATGAGGAG ATTGACAGAG TGATCGGCAA GAACCGGCAG
4921 CCCAAGTTTG AGGACCGGGC CAAGATGCCC TACATGGAGG CAGTGATCCA CGAGATCCAA
4981 AGATTGGAG ACGTGATCCC CATGAGTTG GCCCCCAGAG TCAAAAAGGA CACCAAGTTT
5041 CGGGATTTC TCCCTCCCTAA GGTGCTATCC GCCCCACCC CCCAGACTAC GGGGACTCCA
5101 GCCCCCTCT GTGTCCCCAG CATCCCACCC ACATTAGAAG CTTTCTAGAC CCTGTCCCAC
5161 TCCCTCAATC AGTCAAAAAA GACTTCCCCA ACCACCACAT CCGTTCCACC TTTCCACTTA
5221 GACACTCCTG AGTCCCTGCAT CTCTCCAGAC TCTTTGTGTC AGGAGAATCA AACACATGTT
5281 CCCAAACTTC CTATCTTAAG AAACAGAAGC CCCCTTTCCA TTCGGCCTTT TGTCTAGGG
5341 ACAGAAATCT CAGGTCCCCC AAACCTCTGC CTAGAAGGAC ATGGACCCCA TGTCTCCCAA
5401 ACTTCTGTG TCAGAGATGT GAACCTTCTA TCCCCCAAGG TCCCTCCCTA GAGGTCCCCA
5461 ATTCCCATGC CTGCCACTTC CCTCACCAGG GGCACCCCTAG TTCCCCCTCC AGCCCCCTG
5521 TACTCTCAAC AATCCCCCAA CCGCCTCAT CACATACACC TTCTCTCTCC CTCCCAGGGC
5581 ATAGAAGTGT TCCCTATGTT GGGCTCCGTG CTGAGAGACC TCAGGTTCCT CTCCAACCCC
5641 CGGGACTTCA ATCCCCAGCA CTCTCTGGGT GAGAAGGGGC AGTTTAAGAA GCCTGATGCT
5701 TTTGTGCCCT TCTCCATCAG TAAGAGACCA CTGTTTGGTG CCAGCCTTAC TACTCACACC
5761 AGCAGGGGCC TCCCTTACCC AGTTCCCCCTC TCTGCCGTGT AGCCTAGTAT TTCCCAGCT
5821 TGGCAAGTTC CTGTTAGCAA TCTACCGTCG AGCCACCAGG TGATACTCCC TTAECTACCA
5881 AGCACCCAGT ACCTGTGCCC AGGCAAAAGG AAAGGAAACA TCATACCCCT TTCAGAGGCG
5941 GGGGAAAACC AAAGGCCAGA GAGAATCAGA GATTATTTC CCTAGGTGTA CACAGGAGAT
6001 TCTTCAGCAT CCCTAAAAAG GAGATGACCG CACAGCAGGT CATATTGGG AGTTCTTATC
6061 TGGGGGAAGG GGGATCTTAA ACCTCCCATT GTGGACACCT GGCATCGATC AACCCCATCT
6121 TTTGGTCATC TTTTGGGTCA CTCAAGGAAA CTGAGGTCAA GGAGGCTCAA GAGGCTCCCT
6181 CTTAAAGTCT CTCAGGGCCA TATATTCCAC CCTTCCTCCC TGGGAGAGCC GCAGCTGGAG
6241 GTCGGTACTG GGGCGAGGCT GCACTGAGAG TGGGCTTAC CTCCACCCCT CCCGCTCTC
6301 CTCCTCAGGA AAGCGGAAC GTTTTCGGAGA AGGCCTGCCC AGAATGGAGC TCTTTCTCTT
6361 CTTACACCAC GCATGCAGA ACTTCCGCCT CAAGTCCCTC CAGTCACCTA AGGACATTGA
6421 CGTCTCCCC AAACACGTGG GCTTTGCCAC GATCCCACGA AACTACACCA TGAGCTTCCT
6481 GCCCCGCTGA GCGAGGGCTG TCCCGGTGAA GGTCTGGTGG GCGGGGCCAG GGAAGGGCA
6541 GGGCCAACAC CGGGCTTGGG AGAGGGGCGC AGCTAAGACT GGGGGCAGGA TGGCGGAAAG
6601 GAAGGGGCGT GGTGGCTAGA GGAAGAGAA GAAACAGAAG CGGCTCAGTT CACCTTGATA
6661 AGGTGCTTCC GAGCTGGGAT GAGAGCAAG AAACCCCTTAC ATTATGCTAT GAAGAGTAGT
6721 AATAATAGCA GCTCTTATTT CCTGAGCAGC TACCCCGTGT TCACCTTTGT TCAAAAACCA
6781 TTGCACGCTC ACCTAATTG CCACAAAACC CCCTTCGAAG GGGCGTTCAT GCCCATTTTA

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FIG. 12 (Sheet 2)

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6841 CACGTGACAA AACTGAGGCT TAGAAAGTTG TCTCTGATGT CTCACAAAAC ATAAGTGCCC
6901 AGAAAATCTG CGAACACAGA TCTGTGCCCC TAGCCCTCTA GACAGATTCT TAAAAAGCAC
6961 CTATTCTCTCA CGCAAAACAG TTTAGTATAG AATCACATGG CCTGAACATC CCTGTCCGGG
7021 GGAGTTCCCC AGAGACCTGG GGGGTGGTTG CCCTGCCCTTC ACTGCACACA TGCCCACACT
7081 CTCACCTACT CAACATGCTG TGACTACCCG GGTGTAATCT GTGCTTGCTA CCAGATAAGG
7141 CCACTGTAGC CCATTCAGAG TCAGCCCAGG GACACAACGA GACATCACTG GACATACAGG
7201 GTCAGTCCAT TAACAA

FIG. 12 (Sheet 3)

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CYP2A13 cDNA

5' ATGGCCACCATGCTGGCCTCAGGGCTGCTTCTGGTGACCTTGCTGGCCTGCCT
GACTGTGATGGTCTTGATGTTCAGTCTGGCGGCAGAGGAAGAGCAGGGGGAA
GCTGCTCCGGGAACCCACCCCATTTGOCCTTCATTGGAAACTACCTCCAGCTGAA
CACAGAGCAGATGTACAACCTCCCTCATGAAGATCAGTGAGCGCTATGGCCT
GTGTTCACCATTCACTTGGGGGCCCCGGGGGTGGTGGTGCTGTGGGGACATGAT
GCGGTCAAGGAGGCTCTGGTGGACAGGCTGAGGAGTTCAGCGGGCGAGGCGA
GCAGGCCACCTTCGACTGGCTCTTCAAAGGCTATGGCGTGGCGTTCAGCAACG
GGGAGCGCGCAAGCAGCTCCGGCGCTTCTCCATCGCCACCTAAGGGGTTTTG
GCGTGGGCAAGCGGGCATCGAGGAACGCATCCAGGAGGAGGCGGGCTTCCTC
ATCGACGCCCCCGGGGCAACGCAAGGCGCAATATCGATCCACCTTCTTCCTG
AGCCGCACAGTCTCCAATGTTCATCAGCTCCATTGTCTTTGGGGACCGCTTTGA
CTATGAGGACAAAGAGTTCTGTCACTGTTGCGCATGATGCTGGGAAGGTTT
CAGTTCACGGGAACCTCCACGGGGCAGCTCTATGAGATGTTCTCTTCGGTGAT
GAAACACCTGCCAGGACCACAGCAACAGGCTTTAAGGAGCTGCAAGGGCT
GGAGGACTTCATCGCCAAGAAGGTGGAGCACAACCAGCGCACGCTGGATCCC
AATTCGCCACGGGACTTCATCGACTCCTTTCTCATCCGCATGCAGGAGGAGGA
GAAGAACCCCAACACAGAGTTCTACTTGAAGAACCTGGTGATGAACACCT
GAACCTCTTCTTTGGGGCACTGAGACCGTGAGCACCAACCTGCGCTACGGTTT
CTGTCTGCTCATGAAGCACCCAGAGGTGGAGGCCAAGGTCCATGAGGAGATT
GACAGAGTGATCGGCAAGAACCGGCAGCCCAAGTTTGAGGAACGGGGCCAAG
ATGCCCTACACAGAGGCAGTGATCCACGAGATCCAAAGATTTGGAGACATG
CTCCCCATGGGTTTTGGGCCACAGGGTCAACAAGGACACCAAGTTTCGGGATT
TCTTCCTCCCTAAGGGCACTGAAGTGTTCCCTATGCTGGGCTCCGAGCTGAGA
GACCCACAGGTTCTTCTCCAACCCCCAGGACTGCAGTCCCCAGCACTTCCTGGAT
GAGAAGGGGGCAGTTTAAGAAGAGTGATGCTTTTGTGCCCTTTTCCATCGGA
AAGCGGTACTGTTTTGGAGAAGGCCTGGCCAGAATGGAGCTCTTTCTCTTCT
TCACCACCATCATGCAGAACTTTGGCTTCAAGTCCCCTCAGTCGCTAAGGAT
ATCGACGTGTCCCCAAACAGTGGGCTTTGCCACGATCCACGAAACTACAC
CATGAGCTTCCTGCCCCGCTGAGCGAGGGCTGTGCTGGTGCAGGGCTGGTGGGC
GGGGCCAGGGAAACGGCCCGGGCAGGGGCGGGCTTGTGGGAGGGGGGGGGCT
AAGAATGGGGGCAGTGGGGGAAGGAAGGGGAGAGGTGGTTAGAGGGGAACA
GAAGAAACAGAAGGGGCTCAGTTCACCTTGATGATGTCCTTCAGAGCTGTG
ATGAGAGGAAGGGAAACCTTACAGTATGCTACAAAGAGTAGTAATAATA
GCAGCTCTTATCTCCTGA 3'

FIG. 13

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3421 CCTCCACTTC AGCATCTTCA CCAGCCCCAC TTTATACCTG AGCACCTGAA CAAAAGCCCC
3481 CAATCCAGAC CCAGTAAGTA TCTGGACAGC TGTCTCCAAC CAAGTCCACT TGAATGCCTA
3541 AATACCTAGA CAGGTGCCAC TCACCTCATA CCAGCCCCAC CTGAAGAGCT AAACACCTGG
3601 ACAGGTGTCT TCCAACTCAA CTTCACTTGA ATATCTGAAC ACCTAGATGT GTGCTCCAAT
3661 CCAGCCTCAT TTGCATACCT GAAACCTGGA TATATGCCTC AGTTCTTCTC ACCTAAATTA
3721 CTAGACCGTG CCCCTGGCAC CTAATCCACG TGAAAACTTA GATATAAGTT TCCATCCAAC
3781 CCCACTGAAA TACCTAAACA CCTGGACAGA TGCCTTTAAC TCCGTTCTTT CCTTGCTATG
3841 AAACAAATCC CCATTCCCAT CAGCTCCTGC CCCGTGACAG CTGTCTTCC CTTCCTATCC
3901 TCTCTCTGCA ACCCCAGCTC TATGAGATGT TCTCTTCGGT GATGAAACAC CTGCCAGGAC
3961 CACAGCAACA GGCCTTTAAG GAGCTGCAAG GGCTGGAGGA CTTTCATCGCC AAGAAGGTGG
4021 AGCACAACCA GCGCACGCTG GATCCCAATT CCCCACGGGA CTTTCATCGAC TCCTTTCTCA
4081 TCCGCATGCA GGAGGTACAT CCCAGCAGCC AGTGCAGGCA GGTGCAAAGC CAGGGAGAGG
4141 GAAATCAGGA TGGGAGTGGG GTGGGCAGAC GACACAGGCC CATTCAAATT AGCCCTCGTC
4201 ATAATAATCC TTACAATTGG CCAGGCGGG TGGCTCATGA CCTGTAATCC CAGCACTTTG
4261 GGAGGCCGAG GCAGGTGGAT CACCTGAGGT CAGGAGTTCC AGACCAGCCT GGCCAACATG
4321 GTGAAACCCC GTCTCTACTA AAAATACAAA AATGAGCTAG GTATGGTGGC ATGCGCCTGT
4381 AATCCAGCT ACTCAGGAGG CTGAGACAGA AGAATTTGTT TGAATCCGGG AGGCAGAGGT
4441 TGCAGTGAGC CGGGATCATG CCACTGCACT CCGGCCTGAG TGACAGAGCA AGACCCTGTA
4501 AAAAAAATAA AAAAAAATAA AAAAAATTCC GGAAACCCC AATTACATCA CCCACTGCTG
4561 TCCCATCTAC TGAGCCCTCA CCCACAAGGA CGGGTTATGG AGGTGGATTA GATTGGAAG
4621 AACTTCTCAA GAACCTACCG GTGCCAGGAA CTGGGTAAAG TGTTTTATGA TAGTCCGCCA
4681 TGGAACTT TTAACAGTTC TTGAGGGAGG TTCACTCATG GCCCCAGTTG TACAAATGAC
4741 GAAACTGAGG CCCAGAGAGT TTAAGTGTCT TAACCTGAGT CACAACAGTG AGGAAGACCA
4801 TGGTCCCCCT AGCTCAAACC CTGGTCTCTC TGAGCCTATA GCTGGTGCTT TTAGCCACCA
4861 TGCTCTCTAA CCGTTTCATGT CCTGGTTAGC AGACACACCT CTGTGGACAG GTGACCTGGC
4921 TTTACATTGC AGGGTCCCCG CCTACCTCTG GATGTCAGCC TCCCATGTGG GAAGGCTTTA
4981 GGAAGCCAAA GCTCAGGGAG AAAGGATCAA ATGCTGTGTC TAAAAATTCT GTGCTTGAT CTGAGAAAA
5041 ATTTTTAGGG AAGAAATAGG ATGCTGTGTC TAAAAATTCT GTGCTTGAT CTGAGAAAA
5101 CTCTTTTTTT CTGACTCTTC ATCTTGCCAT CTCTGTACTA CTTTCTCTTC GTCTCCCCTC
5161 ATCTTCTCT CTCCAAATAT TCCTATCATT AAAAAAGTAA CAGACTGGGA AACATGGCAA
5221 AACCCCGTCT GTACAAAAA ATGGCTAGGC ATGGTGGTGC ATGCCTGCCG TCCCAGCTAC
5281 TAAGGAGGTT GAGGTGGGAG GATATCTTGA GCCCAGGGTG GGCAGAGGTT TCAATGAGCC
5341 GATATCACAG CCCTGCCCTC CAGCCTGGGT GACAGAATAA GACCGTGTCT CCCAAAAA
5401 AAAAGAATTA ATTTTTTAAC AGTTAACAA TGAGCCTGCA TAGTCATGTG CATGTGCAGT
5461 TCCAGCTACT CTGGAGGCTG AGACCCGAGG ATTCCTTGAA CCCACGAGTT GGAGTCCAGC
5521 CTGTCCAAC TAGCAAGACC AAGTCTGCAT GATCAGTGAG GTAAAGAAGG TGAGAAGGAA GAGCATTTTG
5581 TTGACAAATTA AAGGATAGAT GATCAGTGAG GTAAAGAAGG TGAGAAGGAA GAGCATTTTG
5641 GGCAAAGCCA GCAGCCAGGG CAAGGGCTGG AACCTGGAGC GAGTTTGGCA AATCTAGGGT
5701 CCCTCTTTCC ACCTTTGGTC TGGACCAAAG AGAGGTAGCT CCAAAGGAAA AGCCCTAGAA
5761 GGGCCCCAAG AGCATGGAGA GTGAGCTTGG TCTAAACCCG CCTCTCCCTG CAGGAGGAGA
5821 AGAACCCCAA CACAGAGTTC TACTTGAAGA ACCTGGTGAT GACCACCCTG AACCTCTTCT
5881 TTGCGGGCAC TGAGACCGTG AGCACCACCC TGGCCTACGG TTTCTGTCTG CTCTGAAGC
5941 ACCCAGAGGT GGAGGGTAAG ACTGGAAAGG GAGGAAAGTG AAGGGCCCCA GACCCTCAAA
6001 ACTCCCTGTA CCTTGGTGCA GTGTACCCAC CTATCCCAGA TCCCAGGACC CTGAGACGTG
6061 CCTTGTCTG CAGAGACAGG ACAATATTCA GCTGATAGGC ATCAGCTCAG TCTCATTAGC
6121 TATTTAAATA TTGAAAATGT CTGCACTGAT TGGTCAGTCA CTCTGTCCC AAGCCCACTG
6181 AGTGTCCGCT GCCTGCTCCT CTGGATCATC CCTTAAGTTC CTCCCTGTG CTACCCCTGTG
6241 ATTCTGACAC AACCTGGTTT AACAGGGATC CTGCTGCAAA CAATGCGAAT GGGTGATGTC
6301 TTGTTCTTGT TTATGAATGG GCTTACCCTT CGTGTCAAGG GTGGAAGCTA TGTCAACCGC
6361 CGTGTTTTAG CTAGGGGGGG CGATACATGC CCTGCTCTAA GACCCCTAGA GAGGGTAAGG
6421 ATATTCCCTT CCTCCGCCAG CCAAGGTCCA TGAGGAGATT GACAGAGTGA TCGGGAAGAA
6481 CCGGCAGCCC AAGTTTGAAG ACCGGGCCAA GATGCCCTAC ACAGAGGCAG TGATCCACGA
6541 GATCCAAAGA TTTGGAGACA TGCTCCCTAC GGGTTTGGCC CACAGGGTCA ACAAGGACAC
6601 CAAGTTTCGG GATTTCTTCC TCCCTAAGGT GCTGTCTCCC CTCCACCACC ACCACTCAGA
6661 CTACGGGGAC TTCCAGCCTC TCTCTGTGTC CCCAGAATCC TGCCCCCATT AGTGTCTAG
6721 ACTCTGTCCC ACTCCCTCAA TCAGTCAAAA AAGACTTCCC CAACCACCAC ATCTGTCTCA
6781 CCTTCCACT TAGACAGTCC TGAGTCTCTG ATCTCGCCAG ACTCTTTGTG TCAGGAGAAT

FIG. 14 (Sheet 1)

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3421 CCTCCACTTC AGCATCTTCA CCAGCCCCAC TTTATACCTG AGCACCTGAA CAAAAGCCCC
3481 CAATCCAGAC CCAGTAAGTA TCTGGACAGC TGTCTCCAAC CAAGTCCACT TGAATGCCTA
3541 AATACCTAGA CAGGTGCCAC TCACCTCATA CCAGCCCCAC CTGAAGAGCT AAACACCTGG
3601 ACAGGTGTCT TCCAACCTCA CTTCACCTGA ATATCTGAAC ACCTAGATGT GTGCTCCAAT
3661 CCAGCCTCAT TTGCATACCT GAAACCTGGA TATATGCCTC AGTTCTTCTC ACCTAAATTA
3721 CTAGACCGTG CCCCTGGCAC CTAATCCAGG TGAAAACTTA GATATAAGTT TCCATCCAAC
3781 CCCACTGAAA TACCTAAACA CCTGGACAGA TGCCTTTAAC TCCGTTCTTT CCTTGCTATG
3841 AAACAAATCC CCATTCCCAT CAGCTCCTGC CCCGTGACAG CTGTCTTCC CTTCCTATCC
3901 TCTCTCTGCA ACCCCAGCTC TATGAGATGT TCTCTTCGGT GATGAAACAC CTGCCAGGAC
3961 CACAGCAACA GGCCTTTAAG GAGCTGCAAG GGCTCGAGGA CTTCATCGCC AAGAAGCTGG
4021 AGCACAACCA GCGCACGCTG GATCCCAATT CCCACGGGA CTTCATCGAC TCCTTTCTCA
4081 TCCGCATGCA GGAGGTACAT CCCAGCAGCC AGTGCAGGCA GGTGCAAAGC CAGGGAGAGG
4141 GAAATCAGGA TGGGAGTGGG GTGGGCAGAC GACACAGGCC CATTCAAATT AGCCCTCGTC
4201 ATAATAATCC TTACAATTGG CCAGGCGCGG TGGCTCATGA CCTGTAATCC CAGCACTTTG
4261 GGAGGCTGAG GCAGGTGGAT CACCTGAGGT CAGGAGTTCC AGACCAGCCT GGCCAAACATG
4321 GTGAAACCCC GTCTCTACTA AAAATACAAA AATGAGCTAG GTATGGTGGC ATGCGCCTGT
4381 AATCCCAGCT ACTCAGGAGG CTGAGACAGA AGAATTTGTT TGAATCCGGG AGGCAGAGGT
4441 TGCAGTGAGT CCGGATCATG CCACCTGCACT CCGGCCTGAG TGACAGAGCA AGACCCTGTA
4501 AAAAAAAAAA AAAAAAAAAA AAAAAATTC GGAAACCCC AATTACATCA CCCACTGCTG
4561 TCCCATCTAC TGAGCCCTCA CCCACAAGGA CGGGTTATGG AGGTGGATTA GATTGGAAG
4621 AACTTCTCAA GAACACCGG GTGCCAGGAA CTGGGTTAAG TGTTTTATGA TAGTCCGCCA
4681 TGAACACTTT TTAACAGTTC TTGAGGGAGG TTCACTCATG GCCCCAGTTG TACAAATGAC
4741 GAAACTGAGG CCCAGAGAGT TTAAGTGTCT TAACTGAGGT CACAACAGTG AGGAAGACCA
4801 TGGTCCCCCT AGCTCAAACC CTGGTCTCTC TGAGCCTATA GCTGGTGTCT TTAGCCACCA
4861 TGCTCTCTAA CCGTTCATGT CCTGGTTAGC AGACACACCT CTGTGGACAG GTGACTTGGC
4921 TTTACATTGC AGGGTCCCCG CCTACCTCTG GATGTCAGCC TCCCATGTGG GAAGGCTTTA
4981 GGAAGCCAAA GCTCAGGGAG AAAGGCTCAA GGGAGCGATT CCTCCACAGT AAGTTTCAAG
5041 ATTTTATGGG AAGAAATAGG ATGCTGTTGC TTAAATTTCT GTGCTTGTAT CTCAGAAAAA
5101 CTCTTTTFTT CTGACTCTTC ATCTTGCCAT CTCTGTACTA CTTTCTCTTC GTCTCCCCTC
5161 ATCTTCTCT TCCAAATAT TCCTATCATT AAAAAAGTAA CAGACTGGGA AACATGGCAA
5221 AACCCCGTCT GTACAAAAAA ATGGCTAGGC ATGGTGGTGC ATGCCTGCGG TCCCAGCTAC
5281 TAAGGAGGTT GAGGTGGCAG GATATCTTGA GCCCAGGGTG GGCAGAGCTT TCAATGAGCC
5341 GATATCACAG CCTGCCCCTC CAGCCTGGGT GACAGAATAA GACCGTGTCT CCCAAAAAA
5401 AAAAGAATTA ATTTTPTAAC AGTTAACAA TGAGCCTGCA TAGTCATGTG CATGTGCACT
5461 TCCACCTACT CTGGAGGCTG AGACCGGAGG ATTCCTTGAA CCCAGGAGTT GGAGTCCAGC
5521 CTGTGCAACT TAGCAAGACC AAGTCTGCAT AAAAAAAAAA AAAACCAACT GACAGCTAAG
5581 TTGACAATTA AAGGATAGAT GATCAGTGAG GTAAAGAAAG GAGCATTTTG
5641 GGCAAAGCCA GCAGCCAGGG CAAGGGCTGG AACCTGGAGC GAGTTTGGCA AATCTAGGGT
5701 CCCTCTTTTC ACCTTTGGTC TGGACCAAAG AGAGGTAGCT CCAAAGGAAA AGCCCTAGAA
5761 GGGCCCCAAG AGCATGGAGA GTGAGCTTGG TCTAAACCGC CCTCTCCCTG CAGGAGGAGA
5821 AGAACCCCAA CACAGAGTTC TACTTGAAGA ACCTGGTGAT GACCACCCTG AACCTCTTCT
5881 TTGCGGGCAC TGAGACCGTG AGCACCACCC TGCGCTACGG TTTCTGTCTG CTCATGAAGC
5941 ACCCAGAGGT GGAGGGTAAG ACTGGAAAGG GAGGAAAGTG AAGGCCCCCA GACCCTCAA
6001 ACTCCCCGTA GCCTGGTGCA GTGTACCCAC CTATCCCAGA TCCCAGGACC CTGAGACGTG
6061 CCTTGCTGTC CAGAGACAGG ACAATATTCA GCTGATAGGC ATCAGCTGAG TCTCATTAGC
6121 TATTAAAAA TTCAAAATGT CTGCACTGAT TGGTCAGTCA CTCTGTCCC AAGCCCCTG
6181 AGTGTCCGCT GCCTGCTCCT CTGGATCATC CCTAAGTTC CTCCCTTGTG CTACCTGTG
6241 ATTCTGACAC AACCTGGTTT AACAGGGATC CTGCTGCAA CAATGCGAAT GGGTGATGTC
6301 TTGTTCTTCT TTATGAATGG GCTTACCCTT CGTGTGAGAG GTGGAAGCTA TGTCAACCGC
6361 CGTGTTTTAG CTAGGGGGGG CGATACATGC CCTGCTCTAA GACCCCTAGA GAGGTAAG
6421 ATATTCCCTT CCTCCGCCAG CCAAGGTCCA TGAGGAGATT GACAGAGTGA TCGCAAGAA
6481 CCGGCAGCCC AAGTTTGAGG ACCGGGCCAA GATGCCCTAC ACAGAGGCAG TGATCCACGA
6541 GATCCAAAGA TTTGGAGACA TGCTCCCCAT GGGTTTGGCC CACAGGCTCA ACAAGGACAC
6601 CAAGTTTCGG GATTTCTTCC TCCCTAAGGT GCTGTCTCCC CTCCACCACC ACCACTCAGA
6661 CTACGGGGAC TTCCAGCCTC TCTGTGTGTC CCCAGAATCC TGCCCCCATT AGTGTCTAG
6721 ACTCTGTCCC ACTCCCTCAA TCAGTCAAAA AAGACTTCCC CAACCACCAC ATCTGTCCA
6781 CCTTTCCACT TAGACAGTCC TGAGTCCTGC ATCTCGCCAG ACTCTTTGTG TCAGGAGAAT

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FIG. 14 (Sheet 2)

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6841 ACACCCZATG TTCCCAATCT TCCTGTCTTA AGAAACAGAA GCCCCCTTTC CATTAGGCCT
6901 TGTGGCTTAG GGACACAAAT CTCAGGTCCC TCAAACACCC TGGCTAGTGG AACATGGACC
6961 CCATGTCTCC CAAACTTCCT GTCTCAGAGA CATGAAACTT CTATCCCCCA AAGCTCCTCC
7021 CTCAGAGGTC CCCAACTCCT CCATGTCTGT CCACTCCCCG CACCTGGGGG ACCCTAGAGC
7081 CCCCTGGAGC CCCTGTGTAC TTTCACCAAT CCCCCCAACC TGGCTCATAA CACACACCTT
7141 CCTCCTCCCT CCCAGGGCAC TGAAGTGTTC CCTATGCTGG GCTCCGAGCT GAGAGACCCC
7201 AGGTTCCTCT CCAACCCCCA GGACTGCAGT CCCCAGCACT TCCTGGATGA GAAGGGGGCAG
7261 TTTAAGAAGA GTGATGCTTT TGTGCCCTTT TCCATCGGTA AGAGACACTG TTTGCTGCCA
7321 GGCCACGGCT CACACCAGCA GGGGCCCTCT TCACCCACCT CCCCTCTCTG CGGTGTAGCC
7381 TGGTATTTCT CCAGCTTGGA AGTTCCTGTT AGAATCTACC ATTGAGCCGC CACCAGCTGA
7441 TACTCCCTTA ACTGCCAAGC ACCCAATACC TGCGCCCAAG TAAAAGGGAA GGAAACATCT
7501 TCCCCATAG ATTTATTTGT CTAGGGTCAC ACAGCAGATT CTTCAGCTCC CTGAAAAGGA
7561 GATAATGGTA CAGCACAGCA GTCATATTTG CATGTGTATC TGGGGGGTAG GGGCATCTAA
7621 ACCTCCCATT GCTACACCTG GCATGGATCA CCCCATCTAT GATGGAGCCA TGACATTATG
7681 CCTTTTTCGA AACCCATAGA ACTGTATAAC ACAGAGTAAA CCCTAATGTA AACTATGGAC
7741 TTTGGTTAGT AATAATATAT CAATATTGGT TCACCATTGT TATATCTCTT ATAGAAGGAA
7801 ACTGAAAGCT AGGGAGGATC GGAGTCTCCT CTGAAAGTCT CTCAGGCCAT AATATTCCCA
7861 CCCCTCCTCC CTAGAGAGTG CAGCCGGGGG TCAGTAGGGG TTGAGGCTGC ACTGAGAGTG
7921 GGCTTCACCT TCACCCCTCC TGCCTCTCCT COTCAGGAAA CCGGTACTGT TTTGGAGAAG
7981 GCCTGGCCAG AATGGAGCTC TTTCTCTTCT TCACCACCAT CATGCAGAAC TTTGCTTCA
8041 AGTCCCCCTA GTCGCCTAAG GATATCGACG TGTCCCCCAA ACACGTGGGC TTTGCCACGA
8101 TCCCACGAAA CTACACCATG AGCTTCCTGC CCCGCTGAGC GAGGGCTGTG CTGGTCCAGG
8161 GCTGGTGGGC GGGGCCAGGG AAACGGCCGG GGCAGGGGGG GGGCTTGTGG GAGGGGGGGG
8221 GCTAAGAATG GGGGCAGTGG GGGGAAGGAAG GGGAGAGGTG GTTAGAGGGA ACAGAAGAAA
8281 CAGAAGGGGC TCAGTTCACC TTGATGATGT CCTTCAGAGC TGTGATGAGA GGAAGGGAAA
8341 CCTTACAGTA TGCTACAAAG AGTAGTAATA ATAGCAGCTC TTATCTCCTG AACAAGTCCC
8401 TCCCTGTGAG CTTTGTTCAG AAAGCGTTGC ACGCTCACCT CACTTATTTG CCACACACCT
8461 CTACCAATGG GGGAAAAGTC TTCATTCCCC TTTTACACG TGAGAAAGGT GCGGCTCAGA
8521 AAGTTGTCTC TATCTGAAAA CTCACAAAAC GCAAGTGTCC AGAGGATCTT GGAACACAGA
8581 TCTGGGCCCC TAGCCCTCTA GATCGATCCT CACCATAGCA CCCCTTCTTC ACGTAAAATA
8641 GCTTAGTATA GCATCACATG GCCTGAACAC CCCTGGGCGG GGGGGTTCCC CAGAGACCTG
8701 GCGGGCGGCT GCCCTGCCTA CTCTGTACAC TCGCCTACTC GGGACCATCC GGGCACCAGG
8761 GTGTACCTG AGCTCGCTA

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FIG. 14 (Sheet 3)

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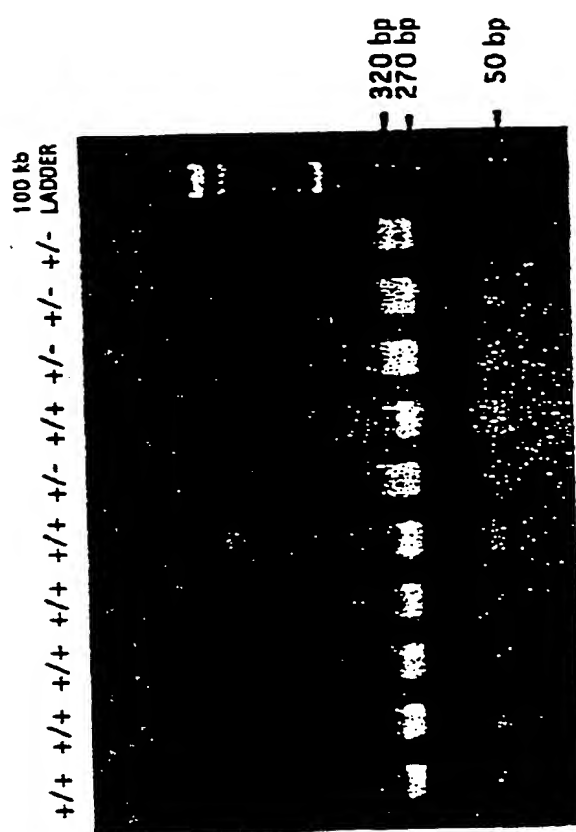


FIG. 15

PCTWORLD INTELLECTUAL PROPERTY
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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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(71) Applicant (for all designated States except US): THE GOVERNMENT OF THE UNITED STATES OF AMERICA, represented by THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES [US/US]; Office of Technology Transfer, National Institutes of Health, Suite 325, 6011 Executive Boulevard, Rockville, MD 20852 (US).

(72) Inventors; and

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(74) Agents: FEILER, William, S. et al.; Morgan & Finnegan, L.L.P., 345 Park Avenue, New York, NY 10154 (US).

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Published*With international search report.**Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.*

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(54) Title: DEFECTS IN DRUG METABOLISM

(57) Abstract

The invention relates to genetic material, and specifically portions of DNA, for identifying the presence or absence of a mutation in the drug metabolism gene CYP2C9 and CYP2A6. Further, the invention comprises a method for determining such mutations and a kit incorporating the genetic material of the invention for performing the said methods so as to determine the presence or absence of mutations in the drug metabolizing gene CYP2C9 and CYP2A6.

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INTERNATIONAL SEARCH REPORT

International Application No.
PCT/US 95/07605

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12Q1/68 C12N9/02 C12P19/34 A61K31/70 C07H21/04
C12N15/55

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12Q C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
T	AMERICAN JOURNAL OF HUMAN GENETICS, vol. 57, September 1995 pages 651-660, FERNANDEZ-SALUERO, P. ET AL 'A genetic polymorphism in coumarin 7-hydroxylation' see the whole document ---	1-6, 8-13, 17, 20
X	WO,A,91 01990 (CITY OF HOPE) 21 February 1991 see page 5 ---	5,6
X	WO,A,94 01548 (MEDICAL RESEARCH COUNCIL) 20 January 1994 see page 364; claim 1 ---	5,6
	-/--	

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

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Date of the actual completion of the international search

30 January 1996

Date of mailing of the international search report

12.02.96

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Osborne, H

INTERNATIONAL SEARCH REPORT

International Application No.

PCI/US 95/07605

C(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	CARCINOGENESIS, vol. 14 , no. 7, July 1993 pages 1421-1427, TIANO, H. ET AL 'retroviral mediated expression of human cytochrome P450 2A6 in CH3/10T1/2 cells confers transformability by NNK.' see the whole document ---	1-4
A	BIOCHEMISTRY, vol. 29, 1990 pages 1322-29, YAMANO S ET AL 'The CYP3A3 gene product catalyses coumarin hydroxylation in human liver microsomes' see the whole document see page 1324, line 1; figure 1 -----	1

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 95/07605

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.: 26-28
because they relate to subject matter not required to be searched by this Authority, namely:
Remark: Although claims 26-28 as far as they concern an "in vivo" method, are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 95/07605

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO-A-9101990	21-02-91	US-A- 5081235	14-01-92
		AU-B- 629401	01-10-92
		AU-B- 6344790	11-03-91
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		DE-D- 69018801	24-05-95
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		EP-A- 0436016	10-07-91
		JP-T- 4502258	23-04-92
		US-A- 5075431	24-12-91
WO-A-9401548	20-01-94	AU-B- 4512193	31-01-94
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